SEARCH REQUEST FORM

Requestor's Name:		Serial Number:	
Date:	, Phone:		Art Unit:
terms that may have a special:	meaning. Give examples or	e specifically as possible the sub r relevent citations, authors, key copy of the broadest and/or most	ject matter to be searched. Define any words, etc., if known. For sequences, relevent claim(s).
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	STAF	F USE ONLY	
Date completed: 07-11 Searcher: Color Terminal time: 200 Elapsed time:	14 @ 4957	Search Site STIC CM-1 Pre-S	Vendors IG STN Dialog
CPU time: 2-6 Total time: 2-6 Number of Searches:	5	Type of Search N.A. Sequence A.A. Sequence	APS Geninfo SDC
Number of Databases:		Structure Bibliographic	DARC/Questel Other CGN

PTO-1590 (9-90)

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July 15, 2002, 12:16:23 ; Search time 58.93 Seconds (without alignments) 1053.627 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2978
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Perfect score:
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A_Geneseq_032802:* Database

7.51051/gggdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Score	Match	Length 1	æ	a	Description	
1 0 0			: :	1		
2978	100.0		17	AAR90619	Sulfolobus solfata	
1748.5	58.7		17	AAR92755	Trehalose-releasin	
1748.5	58.7		17	AAR90620	Sulfolobus acidoca	
1089.5	36.6		22	AAG92072	C glutamicum prote	
1089.5	36.6		22	AAB80206	Corynebacterium ql	
1060.5	35.6		16	AAR77471	Treĥalose releasin	
1058	35.5		16	AAR80290	Trehalose releasin	
1025	34.4		16	AAR80289	Trehalose releasin	
1025	34.4		16	AAR77470	Trehalose releasin	
1024.5	34.4		21	AAY85157	Trehalose-releasin	
1024.5	34.4		21	AAY85165	Trehalose-releasin	
	Score 2978 1748.5 1748.5 1089.5 1060.5 1058 1025 1025 1025 1025 1025	1	1	1	Ouery Match Length DB III 100.0 559 17 P 58.7 556 17 P 58.7 556 17 P 36.6 595 22 P 35.6 598 16 P 35.5 597 16 P 34.4 575 21 P 34.4 575 21 P 34.4 575 21 P	Query Match Length DB ID 100.0 559 17 AAR90619 58.7 556 17 AAR92755 36.6 595 22 AAG92072 36.6 610 22 AAB90206 35.5 597 16 AAR80290 34.4 566 16 AAR80289 34.4 575 21 AAY85165

Sulfolobus spp. derived transferase and amylase - for production of

Bacillus stearothe Starch-branching-e		B.stearothermophil	Propionibacterium	Aquifex aeolicus V	Propionibacterium	S. tuberosum isoam	Heat-resistant pul	C. pneumoniae prot		C glutamicum prote	Corynebacterium gl	Wheat isoamylase p	S. tuberosum debra	a dr		ulanase	Full length Pullul	Zea mays SU1 starc		Bacillus alkaline	Thermotoga maritim	A polypeptide with	Thermotoga maritim	C. pneumoniae prot	Bacillus acidopull	Pullulanase (pulB)	Group B Streptococ	Sequence of amy C	Bacillus deramific	N. denitrificans a	Alpha-glucosidase	Protein encoded by
AAR80037 AAR96109	AAP94635	AAR11271	AAU60903	AAB69074	AAU60913	AAY00870	AAR23787	AAY34991	AAY00869	AAG91100	AAB79423	AAY50819	AAW36602	AAY91279	AAY37184	AAW73552	AAW73553	AAY17523	AAW09257	AAW09255	AAW49871	AAB19285	AAW34567	AAY35095	AAE05691	AAY78513	AAY27357	AAP96105	AAE05719	AAW90977	AAR43340	AAW70886
16	10	12	22	22	22	20	13	20	20	22	22	21	18	21	20	20	20	20	17	17	19	21	18	20	22	21	20	10	22	21	14	19
652 652	648	639	718	630	670	166	628	999	793	731	731	764	909	1250	618	798	1938	818	893	1938	772	621	772	722	829	862	931	498	928	762	555	785
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399 399	385.5	4	$\overline{}$	361	348	348	46	345.5	42	340	340	339	334	333	31	331.5	31	29	29	29	m	312.5	m	60	303.5	03	303	300	299	296	295	294.5
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42		44	45

ALIGNMENTS

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transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose; malto-oligosaccharide; hydrolysis.
                                                                     Sulfolobus solfataricus amylase for alpha, alpha-trehalose prodn.
                AAR90619 standard; Protein; 559 AA
                                                                                                                                                                                    95JP-0120673.
94JP-0133354.
94JP-0194223.
94JP-0290394.
94JP-0286917.
                                                                                                                                                                    95WO-JP01189.
                                                                                                                                                                                                                                  94JP-0311185
                                                    (first entry)
                                                                                                                Sulfolobus solfataricus
                                                                                                                                                                                                                                                    (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                     WPI; 1996-049671/05.
N-PSDB; AAT12325.
                                                                                                                                                                                     21-APR-1995;
15-JUN-1994;
18-AUG-1994;
31-OCT-1994;
                                                                                                                                                                     14-JUN-1995;
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                                                    29-JUN-1996
                                                                                                                                 W09534642-A.
                                                                                                                                                   21-DEC-1995
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                                  AAR90619;
RESULT
AAR90619
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Trehalose-releasing thermostable
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                                               on a saccharide having at least three sugar units, which are pref.
glucose units at the reducing end (the linkage between the first and
second glucose units is alpha-1, while the linkage between the
second and third glucose units is alpha-1,4), to hydrolyse alpha-1,4
linkages within the sugar chain, yielding alpha, alpha-trehalose and also
mono- and disaccharide hydrolysis products. The ampliase has a mal. wt. of
61 to 64 kba. It is characterised by working at pH 4.5-5.5 and at 60-85
deg.C. It has an isoelectric point of 4.3-5.4 and retains at least
100 percent activity after 6 hrs at 80 deg.C. It is completely inhibited
by 5 mm copper sulphate. Use of a transferase and the amylase in
succession on suitable substrates such a malto-oligosaccharides, is
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                                         The amylase acts
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                                                                                                                                                                                                                  100.0%; Score 2978; DB 17; Length 559; 100.0%; Pred. No. 3.6e-236; ive 0; Mismatches 0; Indels 0;
                                       The amylase is derived from Sulfolobus solfataricus.
 alpha, alpha-trehalose from malto-oligosaccharide(s)
                                                                                                                                                                 the production of alpha, alpha-trehalose.
                   Claim 108; Page 235-240; 357pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                           Local Similarity
ses 559; Conserv
                                                                                                                                                                                     559 AA;
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                                                                                                                                                                                      Sequence
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Matches
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DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 IKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGY 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A thermostable enzyme (AAR92755) of Sulfolobus acidocaldarius ATCC 33909 releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of polymerisation of at least 3. It has a mol.wt. of 54 64 kDa (SDS-PAGE), a pl of 5.6-6.6 and is substantially not inactivated when incubated in aq. solution (ph 7.0) at 85 deg for 60 ml. Recombinant enzyme is obtd. by expression of an isolated DNA fragment (AAT16899) in host cells, pref. Escherichia coli, using e.g. vector pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus acidocaldarius, - saccharide at temps. exceeding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pref. Escherichia coli, using e.g. vector pBluescript. The trehelose is useful as a sweetener.
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; Pred. No. 4.1e-135;
87; Mismatches 136;
Sulfolobus acidocaldarius strain ATCC 33909
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant thermostable enzyme from releases trehalose from non-reducing
                                                                                                                                                                                                                                                                                                                                           Sugimoto T;
                                                                                                                                                                                                                                                                                           (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 53-54; 74pp; English
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94JP-0190180.
95JP-0109128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 degrees Centigrade
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11-APR-1995;
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Best Local Simi
Matches 329;
                                             AU9527131-A.
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                                                                                                                                                                                                                                                                                                                                                                                                        302 NIDAQWVDDFHHSIHAYLIGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGEP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 VGELDGCNFVVYIQNHDQVGNRCKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYG 421
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                                                                                                                                                                       122 VIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKK 181
                                                                                                                                                                                                                                                   GLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EENPFYFFSDFSDSKLIQGVREGRKKENGODTDPQDESTFNASKLSWKIDEEIFSFYKIL 481
                                     TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL
                                                                                             DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C glutamicum protein fragment SEQ ID NO: 5826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG92072 standard; Protein; 595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688.
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organic acid synthesis.
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03-AUG-2000;
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Tateishi N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG92072;
                                                                                                                                                                                                                                                                                         182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amylase is derived from Sulfolobus acidocaldarius. The amylase acts on a saccharide having at least three sugar units, which are pref. glucose units at the reducing end (the linkage between the first and second glucose units is alpha-1, while the linkage between the second and third glucose units is alpha-1, while the linkage between the second and third glucose units is alpha-1, while the linkage alpha-1, linkages within the sugar chain, yielding alpha, alpha-trehalose and also mono- and disaccharide hydrolysis products. The amylase has a mal. wt. of 61 to 64 kDa. It is characterised by working at pH 4.5-5.5 and at 60-85 deg.C. It has an isoelectric point of 4.3-5.4 and retains at least 100 percent activity after 6 hrs. at 80 deg.C. It is completely inhibited by 5 mw copper sulphate. Use of a transferase and the amylase in succession on sultable substrates such a malto-oligosaccharides, is useful for the production of alpha, alpha-trehalose.
                                                       | :|| : | | | | : : : : : || | :| ||:
inirkryn-nckrvkevrregncitlimekigiiasfddivinskitgnlligi--gfpk 536
360 vgdlpprkfvvfiqnhdqvgnrgngerlsiltdkttylmaatlyilspyiplifmgeeyy 419
                                                                                                             482 IKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQ 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose; malto-oligosaccharide; hydrolysis.
                                     EENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEIFSFYKIL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus acidocaldarius amylase for alpha, alpha-trehalose prodn.

    for production

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58.9%; Pred. No. 4.1e-135;
.ive 87; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sulfolobus spp. derived transferase and amylase - fo. alpha, alpha-trehalose from malto-oligosaccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 112; Page 244-250; 357pp; Japanese
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                                                                                                                                                                                                                                                                                                                            AAR90620 standard; Protein; 556
                                                                                                                                                                                                             537 klkkdelikvnrgvgyygl 555
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94JP-0133354.
94JP-0194223.
94JP-0290394.
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94JP-0311185
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Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus acidocaldarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIRI ) KIRIN BEER KK
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31-OCT-1994;
21-NOV-1994;
21-NOV-1994;
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15-JUN-1994
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Yokoi

Sequence

Query Match

AAB80206 standard; Protein; 610 AA.

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; SEQ ID NO: 5826; 246pp + Sequence Listing; English.
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N-PSDB; AAH67291
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36.6%; Score 1089.5; DB 22; Length 595; 41.5%; Pred. No. 6.5e-81; .ive 93; Mismatches 198; Indels 29; Gaps 11; DGFRLDAVHAIIDTSPKHILEEIADVVHKYN-----RIVIAESDLNDPRVVNPKEKCGY 301 YLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVIL 187 DVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYNV 247 385 vhpditpasrfytyttthdqtgnraigdrpsttltpeqqvlkaaiiysspytpmlfmgee 444 420 YGEENPFYFFSDFSDSKLIQGVREGRKKE-----NGQD-TDPQDESTFNASKLSWKIDE 472 PASRYQPEGVHGPSQIIQESKEFNNETFLKK -- EDLIIYEIHVGTFTPEGTFEGVIRKLD 127 362 VGE--LDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEE 419 :| || || :| :| :| ||||:| fgattpfaffcshtdpelnrltsegrkrefarlgwnaddipspelestftsskldwefta 504 E---IFSFYKILIKMRKELSIACDR--RVNVVNGENWLIIKGREYFSLYVFSKSSIEVKY 527 FTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE----IPD 69 fsvwaplphdvhl-ilngetlpmhktegswwraei-apkagdrygfslfdgsswsktlpd 85 Query Match Best Local Similarity 41.5% Matches 227; Conservative 528 SGTLLLS 534 ggeliys 571

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RESULT AAB80206

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fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
                                                                 Corynebacterium glutamicum; metabolic pathway protein; MP protein;
                                                 Corynebacterium glutamicum MP protein sequence SEQ ID NO:1146
                                                                                                  carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                                                                  99DE-1031465.
99DE-1031478.
99DE-1031510.
99DE-1031541.
99DE-1031573.
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99DE-1031418.
99DE-1031420.
99DE-1031424.
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99DE-1032125.
99DE-1032130.
99DE-1032130.
99DE-1032186.
99DE-103220.
99DE-1032227.
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99DE-1031453.
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99US-0148613.
99DE-1040764.
99DE-1040765.
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99DE-1031634
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99DE-1042079
                                                                                                                 Corynebacterium glutamicum
                                (first entry)
                                                                                                                                 WO200100843-A2
                                                                                                                                                                                                                                                                 08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                30-APR-2001
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08-JUL-1999;
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               AAB80206;
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VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                        AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, uncleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                    pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | ||:|||| |:: :| | : : : : :||:|||||: || prstsqpdgynglsevsddsylwgdqqwtgrilpgsvlyelhvgtfsedgtfegvvdklp 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || |||||||: | :| :| | :| | dglrldavhslddrgaysllagltmvaedvsaqtgiprsliaeselndpkfvtsreaggf 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGEENPFYFFSDFSDSKLIQGVREGRKKE-----NGQD-TDPQDESTFNASKLSWKIDE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PASRYQPEGVHGPSQIIQESKEFNNETFLKK -- EDLIIYEIHVGTFTPEGTFEGVIRKLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVIL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGFRLDAVHAIIDTSPKHILEEIADVVHKYN-----RIVIAESDLNDPRVVNPKEKCGY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE----IPD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 NIDAQWVDDFHHSIHAYLTGEROGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRKTHGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYNV
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                                                                                                                                                                                                             Nucleic acids from Corynebacterium glutamicum encoding metabolic
                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 610;
                                                                                                                                         Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1089.5; DB 22;
; Pred. No. 6.7e-81;
93; Mismatches 198; II
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                                                                                                                                         Zelder
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                                                                                                                                         Η,
                                                                                                                                         Schroeder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%;
41.5%;
           99DE-1042087.
99DE-1042088.
99DE-1042095.
99DE-1042124.
99DE-1042129.
2000US-0187970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 36.6%
Best Local Similarity 41.5%
Matches 227; Conservative
                                                                                                                                         В,
                                                                                                                                          Kroeger
                                                                                                                                                                   2001-137957/14
                                                                                                                                                                                                                                                                                                                                                                                                                             610 AA;
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N-PSDB; AAF72325
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                                                                                                             (BADI ) BASE
                                                                  03-SEP-1999;
09-MAR-2000;
                          03-SEP-1999
                                      03-SEP-1999,
                                                      03-SEP-1999;
                                                                                                                                       Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                      Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose; alpha-maltotriosyltrehalose; alpha-maltoterrasyltrehalose; maltopentaosyltrehalose; sweetener; taste-improving agent; stabiliser; filler; exclient; adjuvant; foodstuffs; cosmetics;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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from a non-reducing saccharide having a trehalose structure as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.6e-78;
2; Mismatches 197; Indels
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                                                                                                                                 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 27-29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                         AAR77471 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94JP-0059840
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                                                                                                                                                                                                                                                                                      Trehalose releasing enzyme.
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232; Conser
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586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceuticals.
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580 ggeliys
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                                                                                                                                                                                                                                  25-JAN-1996
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408
NFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRI 280
                                                          281 V-----IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLD 334
                                                                                                                335 DIVKSYKDVFVYDGKYSNFRKTHGEPVGELDGCNF------VVYIQNHDQVGNRGKG 386
                                                                                                                                                                                                                  ERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRK 446
                                                                                                                                                                                                                                             drlsqtlpygslalaavltltgpftpmllmgeeygastpwqfftshpepelgkataegri 468
                                                                                                                                                                                                                                                                          447 KE---NGQD----TDPQDESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-- 492
                                                                                                                                                                                                                                                                                                      469 kefermgwdpavvpdpgdpetfrrskldwaeaaegdharllelyrsltalrrstpdltkl 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a trehalose releasing enzyme - which releases trehalose from a non-reducing saccharide having a trehalose structure as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose; alpha-maltotriasyltrehalose; alpha-maltotriasyltrehalose; maltopentaosyltrehalose; sweetener; taste-improving agent; stabiliser; filler; exciplent; adjuvant; foodstuffs; cosmetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This enzyme can be used for the preparation of trehalose with high yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltoxyltrehalose, alpha-maltotresyltrehalose and alpha-maltotriosyltrehalose. The trehalose can be used as a sweetener,
                                                                                                                                                                          | :| || : | || 529 gfedtqvafdedarwlrfrrggvqvllnfseqpvsldgagtall
                                                                                                                                                                                                                                                                                                                                 --- DRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 24-25; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR80290 standard; Protein;
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94JP-0059834.
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                                                                                                                                                                                                                                   119 FEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEA 178
                                                                                                                                                                                                                                                  HKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENV 238
                                                                                                                                                                                                                                                                                                                                           EYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIV-----IAESDLNDPRV 292
                                                                                                                                                                                                                                                                                                                                                          293 VNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSN 352
                                                                                                                                                                                                                                                                                                                                                                                                       petfrrskldwaeaaegdharllelyrsltalrrstpdltklgfedtqvafdedarwlrf 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRRKTHGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAAL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 YLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQD 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-----DRRVNVVNGENWLII 507
taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
                                                                                                      Gaps
                                                                                                                              14 FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTI----TLNNVKVRDRYKYVLD 62
                                                                                                                                             Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose; alpha-maltotriosyltrehalose; alpha-maltoterizasyltrehalose; maltopentaosyltrehalose; sweetener; taste-improving agent; stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
                                                                                                                                                                                                Length 597
                                                                         35.5%; Score 1058; DB 16;
40.5%; Pred. No. 2.5e-78;
ive 88; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 KGREYFSLYVFSKSSIEVKYSGTLLL 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 589
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                                                                                                    Matches 229; Conservative
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                                                                                        Similarity
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                                      AA;
                                    597
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                                      Sequence
                                                                          Query Match
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                                                                                        Best Local
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13-SEP-1995
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Best Local Si
Matches 229;
                                                                                                         AAR77470;
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                                           AAR77470
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plpdprtrrqpegvhalsrtfdpgahrwgdagwggrelqgsviyelhigtftpeqtldaa 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : || : || ||||||:| ::|| |||:|| :| :| || :|| ||:|| :
dvngyglagqwsddfhhavhvnvsgettgyysdfdslgalakvlrdgffhdgsyssfrgr 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THGEPVGELDGCNF------VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
                                                                                                                                                                                                                                                                                                                                                                                             yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose, alpha-maltotriosyltrehalose, alpha-maltoternasyltrehalose and maltopentaosyltrehalose. The trehalose can be used as a sweetener, taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                        releases trehalose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a trehalose releasing enzyme – which releases trehalc
from a non-reducing saccharide having a trehalose structure as an
end unit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYNVDGFRLDAVHAIIDTSPKHILEE---IADVVHKYN---RIVIAESDLNDPRVVNPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                            enzyme can be used for the preparation of trehalose with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 1.3e-75; 80; Mismatches 197;
                                                                                                                                                Sugimoto T, Tsusaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.4%; Score 1025; 40.3%; Pred. No. 1.
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                                                                                                     (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 21-22; 45pp; English
  95EP-0301474
                                           94JP-0059840
94JP-0059834
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                                                                                                                                                Kubota M,
                                                                                                                                                                                   WPI; 1995-312772/41.
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nes 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 AA;
                                                                                                                                                                                                          N-PSDB; AAQ98669
07-MAR-1995;
                                        07-MAR-1994;
07-MAR-1994;
                                                                                                                                                Hattori K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 KEYNVDGFRLDAVHAIIDTSPKHILEE---IADVVHKYN---RIVIAESDLNDPRVVNPK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This enzyme can be used for the preparation of trehalose with high yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose, alpha-maltotetrasyltrehalose and maltopentacosyltrehalose. The trehalose can be used as a sweetener, taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                             trehalose; alpha-qlucosyltrehalose; alpha-maltosyltrehalose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fdiwapeagtvtl--laggeryemgrrpgngpadegwwtaadaptgadvdygylldgdei
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                                                                                                                                                                                                                                alpha-maltotriosyltrahalose; alpha-maltoterrasyltrehalose;
maltopentaosyltrehalose; sweetener; taste-improving agent;
stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNA encoding a trehalose releasing enzyme – which releases treh
from a non-reducing saccharide having a trehalose structure as
end unit.
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Pred. No. 1.3e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugimoto T,
     ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 27-29; 45pp; English.
  296
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40.38;
AAR77470 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0059840.
94JP-0059834.
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                                                                                                                                                          Trehalose releasing enzyme.
                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-312772/41
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                                                                                                                                                                                                                                                                                                              pharmaceuticals
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                                                                                                      25-JAN-1996
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us-09-298-924-6.rag

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This sequence represents a trehalose-releasing enzyme amino acid sequence from Arthrobacter sp. S34. This enzyme specifically hydrolyses a non-reducing saccharide having a trehalose structure as an end unit. The invention relates to this enzyme and also to a non-reducing saccharide forming enzyme that forms a non-reducing saccharide having a trehalose structure as an end unit by reducing partial starch hydrolysates. The two enzymes can be used to produce trehalose, a disaccharide consisting of two moles of glucose bound at their reducing residues. The disaccharide is substantially free of reducibility and has moisture retaining abilities. The enzymes are used to produce non-reducing sugars, they are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mesophilic enzyme from Arthrobacter, used to convert starch hydrolysate into non-reducing sugars, particularly trehalose, useful as a sweetener in foods, pharmaceuticals and cosmetics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-reducing saccharide-forming enzyme; trehalose; disaccharide; food; high yield; trehalose releasing enzyme; moisture retention; cosmetic;
                                                                                                                                                                                            488
EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRK 356
                                                             357 THGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
                                                                                                                                                                461
                                                                                                                                                                                                                          NASKLSWK-----IDEEIFSFYKILIKMRK-----ELSIACDRRVNVVNGENWLIIKGR 510
                                                                                                                     PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miyake T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trehalose-releasing enzyme amino acid sequence.
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                                                                                                                                                                                                                                                                                   511 EYFS----LYVFSKSSIEVKYSGTLLL 533
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                                                                                                                                                                                                                                                                                                                                                                                    AAY85157 standard; protein; 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-0258394.
98JP-0352252.
99JP-0016931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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N-PSDB; AAA10503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arthrobacter
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26-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production.
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13;
particularly used for further enzymatic conversion of starch hydrolysate to trehalose. The non-reducing sugars produced by the enzymes are useful in foods, pharmecuticals and cosmetics. Non-reducing sugars are compatible with amino acids and proteins, they do not cause browning, and have good moisture-retaining properties. The enzymes produce the non-reducing sugars in high yield and function at a medium temperature range i.e. between 40 degrees celsius and 60 degrees celsius, and in an acidic pH range, i.e. a pH of less than 7 Production of non-reducing sugars using the enzymes aliminates the need to convert a starch by decological acidic (non-reducing) by catalytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA----DVVHKYNR--IVIAESDLNDPRVV 293
                                                                                                                                                                                                                                                                                                               FTLWAPYQKSVKLKVLEKGLYE--MERDEKGYFTITL---NNVKVRDRYKYVLDDASEIP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mlfingeewgartpwqfftshpepelgeatargriaefarmgwdpavvpdpqdpatfarsh
                                                                                                                                                                                                                                                                                                                                                        DPASRYQPEGVHGPSQIIQESKEFNNETFLKKED------LIIYEIHVGTFTPEGTF
                                                                                                                                                                                                                                                                                                                                                                                                                 EGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 NPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRKTHGEPVG-ELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTFNASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSWKIDEE-----IFSFYKILIKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSK
                                                                                                                                                                                                                                  575;
                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                              189; Indels
                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                Score 1024.5; DB :
Pred. No. 1.4e-75;
; Mismatches 189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rehalose-releasing enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-reducing saccharide-forming enzyme; high yield; trehalose releasing enzyme; production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY85165 standard; Protein; 575
                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                  34.48;
39.48;
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                     AA;
                                                                                                                                                                                     575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 SSIEV 525
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                                                                                                                                                       nydrogenation
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                                                                                                                                                                                     Sequence
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ywlrdmhadglrldavhalrdaralhlleelaarvdelagelgrpltliaesdlndpkli 296
                                                                                                                                                                                                                                             mlfmgeewgartpwqfftshpepelgeatargriaefarmgwdpavypdpgdpatfarsh 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A gene coding for a thermostable branching enzyme has been isolated from chromosomal DNA of B.stearothermophilus strain TRBE14 and sequenced (see AAT04542). The enzyme (AAR80037) was found to have an activity of 80% or more at up to 65 deg.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AYKIDGNEVI-----FTLWAPYQKSVKL----KVLEKGLYEMER-DEKGYFTITLN 49
                                        294 NPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNF
                                                             MIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTFNASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable branching enzyme gene and recombinant plasmid contg. - used to produced a thermostable branching enzyme
                                                                                                                         RRKTHGEPVG-ELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP
                                                                                                                                                                                                                                                                                     LSWKIDEE-----IFSFYKILIKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Mismatches 189; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Met residue corresponds to TTG codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable; 1,4-alpha-glucan; branching enzyme; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus thermostable branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%; Score 399; DB 16; 25.2%; Pred. No. 4.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus stearothermophilus (strain TRBE14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR80037 standard; Protein; 652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 6-12; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0311004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0311004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 25.29
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amylopectin; transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-315926/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT04542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                      521 SSIEV 525
                                                                                                                                                                                                                                                                                                                                                                                                           gplrv 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07213287-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR80037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a trehalose-releasing enzyme amino acid sequence from Arthrobacter sp. S34. This enzyme specifically hydrolyses a non-reducing saccharide having a trehalose structure as an end unit. The invention relates to this enzyme and also to a non-reducing saccharide forming enzyme that forms a non-reducing saccharide having a trehalose structure as an end unit by reducing partial starch hydrolysates. The two enzymes can be used to produce trehalose, a disaccharide consisting of two moles of glucose bound at their reducing residues. The disaccharide is substantially free of reducibility and has moisture retaining abilities. The enzymes are used to produce non-reducing sugars, they are particularly used for further enzymatic conversion of starch hydrolysate to trehalose. The non-reducing sugars are useful.

In foods, pharmaceuticals and cosmetics. Non-reducing sugars are useful in foods, pharmaceuticals and cosmetics. Non-reducing sugars are compatible with amino acids and proteins, they do not cause browning, and have good moisture-retaining properties. The enzymes produce the con-reducing sugars in high yield and function at a medium temperature acidic pH range, i.e. a pH of less than 7. Production of non-reducing sugars using the enzymes claimates the need to convert a starch hydrolysate into sugar alcohols (non-reducing) by catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                      hydrolysate into non-reducing sugars, particularly trehalose, useful as a sweetener in foods, pharmaceuticals and cosmetics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPASRYQPEGVHGPSQIIQESKEPNNETFLKKED------LIIYEIHVGTFTPEGTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dprslrqprgvh----elgrefdparyawgddgwrgrdltgaviyelhvgtftpegtl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGVIRKLDYLKDLGITA1EIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 KKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA----DVVHKYNR--IVIAESDLNDPRVV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :||| | | | : :| | : ||| | :|| fpvwapqaaqytl-vvgqgraelpltrdengwwalqqpwdggpdlvd-ygylvdgkgpfa 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 FILWAPYQKSVKLKVLEKGLYE - - MERDEKGYFTITL - - - NNVKVRDRYKYVLDDASEIP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189; Indels
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                                                                                                                                                                                                                                                                                                        Kubota M, Fukuda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6-2; Page 56-58; 93pp; English.
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-:
-:
                                                                                                                                                                                                                                                              (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
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                                                                                                                                                                            98JP-0258394.
98JP-0352252.
99JP-0016931.
                                                                                                                                        99EP-0307220.
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                 Arthrobacter sp. S34
                                                                                                                                                                                                                                                                                                        famamoto T, Maruta
                                                                                                                                                                                                                                                                                                                                                 2000-273225/24
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                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA10516.
                                                                                                                                        13-SEP-1999;
                                                                                                                                                                                 11-SEP-1998;
                                                                                                                                                                                                  11-DEC-1998;
26-JAN-1999;
                                                       EP990704-A2
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Best Local Simi
Matches 215;
                                                                                                  05-APR-2000
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                                                        ----EDLIIYEIHVGTF-TPEGTF----EGVIRKLDYLKDLGITAIEIMPIAQFPGKRD 150
                                                                                          206
                                                                                                   259
                                                                                                                                                                        372 VYIQN-----HDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYI-----PMIFMGEE 419
                                                                                                                                                                                                                                         50 NVKVRDRYKY--VLDDASEI--PDPASRYQPEGVHGPSQIIQESK--EFNNETFLKK--- 100
                                                                                                                                                            -----DISPKHILEEIADVVHKY--NRIVIAESDLNDPRVVNPKEKCGYNIDAQWVDDF 311
                                                                                                                                                                                              HHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNFV 371
                                                                                                                                                                                                                                                                420 YGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEI---- 474
                                                                                                                                                                                                                                                                                  ------- 482
:|:: | || syelfgahvineggkvgtrfcvwapharevrlvgsfndwdgtdfrlekvndegvwtivvp
                                  Escherichia coli;
food-additive;
                                                                                          WGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GPEGNYMVKLGP--
                                                                                                                                    -YFSQKYKT -- PWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAII----
                                                                                                                                                                                                                                                                                                 475 -FSFYKILIKMRKELSIACDRRVNV-----NGENWLIIKGREYFSLYVF 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709..317
/note= "Conserved amylase sequence"
414..423
/note= "Conserved amylase sequence used to
construct primer AAT27127"
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                                                                                                                                                                                                                                                                                                           | :: : | || || || || 483 dfelhrkmndymkel-iacykrykpfyeldhdpqgfewldvhnaeq-sifsf
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus stearothermophilus strain TRBE14 (FERM P-13916).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238..249
/note= "Conserved amylase sequence used
construct primer AAT27126"
                                                                                                                                                                                                                                                                                                                                                                                                                            Starch-branching-enzyme; thermostable; Q-enzyme; starch; amylopectin; glucan; cyclodextrin; food; adhesive; biodegradable plastic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           AAR96109 standard; Protein; 652 AA
                                                                                                                                                                                                                                                                                 ------faqfde------
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                                                                                                                                                                                                                                                                  Takaha T;
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                                                                                                                                                                                                                                                                  Okada
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                                                                                                                                                                                                                                                                  Nakamura
                                                                                                                                                                                                                                                           Imanaka T, Nakamura
Terada Y, Yanase M;
94JP-0218554.
                                                                                                                      (EZAK ) EZAKI GLICO CO LTD.
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13-SEP-1994;
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Matches 149;
                                                                                                                                                                                                                                                           Fujii K, l
Takata H,
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                                  WGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GPEGNYMVKLGPYF
                                                                                                                   SQKYK-----TPWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAII----
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thermostability, for use in modifying starch-like substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid bacteria, esp. Lactobacillus plantarum and E. faecalis, transformed with an exogenous DNA encoding an enzyme which breaks down an oligosaccharide and/or a polysaccharide into a fermentable carbohydrate. The exogenous enzyme is especially an alpha-amylase (AAP94635) encoded by the DNA sequence in AAN91246 (Claims 2, 6 and 10). The transformed lactic acid bacteria can break down polysaccharides and oligosaccharides in a silage crop to provide a complete source of the fermentable carbohydrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Josson K;
    --wkfedeldwylf 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that the Pactic acid bacteria need for producing lactic acid. Also claimed is a probiotic characterised by the transformed lactic acid bacteria which can be used for establishing and maintaining optimal intestinal flora in animals, including humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVKVRDRYKYVLD----DASEIPDPASRYQPEGVHGPSQIIQ-ESKEFNNETF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim an inoculum for silage which comprises lactic
                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus plantárum; E. faecalis;
Bacillus thuringiensis strain H1.1 serotype H1 var thuringiensis.
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                                           -FSFYKILIKMRKELSIACDRRVNVV-----NGENWLIIKGREYFSLYVF 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transformed lactic acid bacteria -
using exogenous DNA hich codes enzyme that breaks down
oligosaccharide and/or polysaccharide, used in silage or as
probiotic
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                                                                                                                                                                                                                                                                                                                                                                                Alpha-amylase; silage; probiotic; lactic acid bacteria;
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encoded by the glgB gene. It is stable at high temps. and can be produced in large amts. using recombinant techniques. It is a transferase allowing formation of alpha(1-6) branches in starch-like substances. It is useful for extending the shelf life of such materials and can be used in the prepn. of human and animal foods.
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22 syelfgahvikkngmygtrfcvwapharevrlygsfnewngtnfnlmkvsnggvwmifip 81
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455 pgkkllfmggefgg-----fdewkd------
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Best Local Similarity 23.6 Matches 141; Conservative
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Search completed: July 15, 2002, 12:17:32 Job time: 69 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Issued_Patents_AA:*

Database

Appli Appl Appli Appli Appli Appl Appl Appl Sequence 1, Appendix No. 1, Ap Sequence 15, Description Sequence 1 Sequence 2 Sequence 4 Sequence 2 Sequence 2 US-09-242-690A-15 US-08-798-269-1 US-08-798-269-1 US-08-798-269-1 US-08-798-646-14 US-08-961-240-14 US-08-961-240-14 US-08-961-240-14 US-08-961-240-14 US-08-961-240-14 US-08-961-240-12 US-09-514-302-2 US-08-410-784A-2 -09 - 346 - 237 - 10SUMMARIES DB Length Query Score 1748.5 1748.5 1060.5 1060.5 1060.5 1060.5 1059.6 1025.6 10 Result Š.

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Sequence 11, Appl Sequence 4, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 3, Appli	OF PRODUCING PROTEINS USING THE CALLED ALONG PROTEINS USING THE CALLED ALONG PROTEINS USING THE CALLED PROTEIN AI Sequence: Synthetic protein	tch al Similarity 100.0%; Score 2978; DB 4; Length 559; 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MTFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMBENDEKGYFTITLNNVKNEDRYKYV 60
4 US-09-346-237-11 2 US-08 410-784A-4 4 US-09-514-599-6 4 US-09-614-599-6 1 US-08-039-777-3 1 US-08-611-361A-3 4 US-09-514-599-2 4 US-09-514-599-4 1 US-08-474-140-11 1 US-08-477-630-11 1 US-08-477-630-11 2 US-08-477-630-11 3 US-08-474-545-11 3 US-08-6733-11 3 US-08-6733-11 3 US-08-6733-11 3 US-08-673-11-13 4 US-08-537-002A-3 4 US-08-537-002A-3 3 US-08-637-002A-3	METHOD OF 2,690A 2924	100.0%; Score 2978; D 100.0%; Pred. No. 4.1e iive 0; Mismatches mapyQKSVKLKVLEKGLYEMERD [
329.5 11.1 818 321.5 10.8 740 303.5 10.2 829 303.5 10.2 829 293.5 9.9 921 291.9 9.8 921 286 9.6 928 286 9.6 928 286 9.6 928 286 9.6 928 286 9.6 928 285 9.6 928 285 9.6 928	DA-15 5. Applicatic 6.24534 ORMATION: 1. KONDO, KEIJ 1. KONDO, KEIJ 1. WENITON: YE INVENITON: YE INVENITOR: YE INV	tch 559; Conservative MTFAYKIDGNEVIFTLWAP H
00010m4000m044444 00010m4000m0444444	RESULT 1 US-09-242-690 Sequence 15 Patent No. Patent No	Ouery Match Best Local Matches, 55 Qy 1 MTF Qy 61 LDD Qy 121 GVI Qy 121 GVI Qy 181 KGL Db 181 KGL

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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                  PVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEY
                                                                                                                                                                                                 LIKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION VUMBER: US/08/505,377
FILING DATE: 21-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 43.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 190180/1994
FILING DATE: 21-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 109128/1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MITSUZUMI=1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08505377
Patent No. 5856146
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MITSUZUMI, Hitoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
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(202) 737-3528
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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REGISTRATION NUMBER: 2
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; MOLECULE TYPE: protein
US-08-505-377-1
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Fatent No. 6027918
GENERAL INFORMATION:
APPLICANT: MITSUZUMI, Hitoshi
APPLICANT: MISUZUMI, Hitoshi
APPLICANT: KUBOTA, Michio
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                             242 IKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGY 301
                                                                                            3 SFGCNIEKKNGIFKLWAPYVNSVKLK-LSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII 61
                                                                       TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL 61
                                                                                                                                                                                                                                       182 GLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYW
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                                   7;
 Length 556;
                                   Indels
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; Score 1748.5; DB 2;
; Pred. No. 1.9e-143;
87; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
58.7%;
58.9%;
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                                   Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                  Similarity
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                                   329;
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Query Match
Best Local S
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APPLICANT: MITSUZUMI, Hitoshi
APPLICANT: KUBOTA, Michio
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: RECAMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING SACCHARIDE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG 121
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58.9%; Pred. No. 1.9e-143;
ive 87; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/505,377
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 109128/1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MITSUZUMI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 1, Application US/09055210 Patent No. 6346394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25,618
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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(202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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Matches 329; Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-09-055-210-1
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MEDIUM TYPE: Floppy
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                                                                              GENERAL INFORMATION:
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         RESULT 4
US-09-055-210-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.7%; Score 1748.5; DB 3; Length
58.9%; Pred. No. 1.9e-143;
tive 87; Mismatches 136; Indels
                                 FILING DATE: 21-JUL-1995
APPLICATION NUMBER: JP 191080/1994
FILING DATE: 21-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 109128/1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLOWDY, ROGEL L
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MITSUZUMI=1
TELECOMMUNICATION INFORMATION:
                     US/08/505,377
                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 628-5197
TELEFAX: 24068
TELES: 24968
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 556 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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Best Local Similarity
Matches 329; Conserv
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MOLECULE TYPE:
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APPLICANT: KUBOTA, Michio
APPLICANT: TSUSARI, Kelji
APPLICANT: TSUSARI, Kelji
APPLICANT: HYTORI, Kazuko
APPLICANT: HYTORI, Kazuko
APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
            301
                                                                      361
                                                                                      541
                                                                                                                                                                                                                                                                        VGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYG 421
                                                                                                                                                                                            EENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWXIDEEIFSFYKIL 481
                         482 IKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQ
           242 IKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGY
                                                                   302 NIDAQWVDDFHHSIHAYLIGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUBOTA=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08399646 Patent No. 5556781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: KT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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amino acid
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APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOSHIJUKI
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 NFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRI 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 DIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNF------VVYIQNHDQVGNRGKG 386
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                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                   47 --TLNNVKVRDRYKYVLD-DASEIPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKKE- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 QGAVIYELHLGTFTPEGTLEAAAGKLDYLAGLGVDFIELLPVNAFNGTHNWGYDGVQWFA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 V----IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLD 334
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                                                                                                                                                                                                   1 MTFAYKIDGNEVI-----FTLWAPYQKSVKLKVLEKG-LYEMER------DEKGYFTI-- 46
                                                                                                                                                                                                                             161 VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTF
                                                                                                                                                    63;
                                                                                                  Length 598;
                                                                                             35.6%; Score 1060.5; DB 1; Length 39.7%; Pred. No. 1e-83; ive 92; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 --- DRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLL 533
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08607321
Patent No. 5716813
                                                                                                                       Best Local Similarity 39.79
Matches 232; Conservative
protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
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D.C.
USA
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GENERAL INFORMATION:
APPLICANT: KUBGTA, Michio
APPLICANT: TUSAKI, Keiji
APPLICANT: TUSAKI, Kazuko
APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENXWE, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TLNNVKVRDRYKYVLD-DASEIPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKKE- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 -DLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTFAYKIDGNEVI-----FTLWAPYQKSVKLKVLEKG-LYEMER------DEKGYFTI-- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTHTYPREAAKPVLGPARYDVWAPNAESVTL---LAGGERYAMORRAETGPEDAGWWTAAG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.6%; Score 1060.5; DB 2; Length 598; Best Local Similarity 39.7%; Pred. No. 1e-83; Matches 232; Conservative 92; Mismatches 197; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                             STREET: 419 Seventh Street, N.W., Suite 300 STATE: 0.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/961,240 FILING DATE: 30-OCT-1997 CLASSIFICATION: 435
                                                       Sequence 14, Application US/08961240 Patent No. 5830715
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 598 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                      US-08-961-240-14
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                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
      линея: US/08/607,321
26-FEB-1996
                                                                                                                                                                                                                                                                                              KUBOTA=5
                                                                                                                                APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 598 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.79
Matches 232; Conservative
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                       CLASSIFICATION:
                                      FILING DATE:
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                                                                                          Query Match
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                                                                                                         Best Local
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APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATONE, Kasuko
APPLICANT: HATONE, Kasuko
APPLICANT: SUGTHOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                         281 V------IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLD 334
                                                                                       335 DIVKSYKDVFVYDGKYSNFRKTHGEPVGELDGCNF-----VVYIQNHDQVGNRGKG 386
                                                                                                                                                     ERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRK 446
                                                                                                                                                                                                                 469 KEFERMGWDPAVVPDPQDPETFRRSKLDWAEAAEGDHARLLELYRSLTALRRSTPDLTKL 528
                                                                                                                                                                                                                                                             KE---NGQD----TDPQDESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-- 492
        NFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRI
                                                                                                                                                                                                                                                                                                                       --- DRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLL 533
                                                                                                                                                                                                                                                                                                                                                     529 GFEDTQVAFDEDARWLRFRRGGVQVLLNFSEQPVSLDGAGTALL 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPALIZATION CONTRACTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/605,501 FILING DATE: 26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION: 435
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUBOTA=5
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08605501 Patent No. 5834287 GENERAL INFORMATION:
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25,618
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 598 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 419 Sever CITY: Washington STATE: D.C.
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Patent No. 5556781
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: HATTORI, Kazuko
APPLICANT: SIGIMOTO, TOSHIJUKi
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                              102 -DLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYA 160
                                                                                                                                                                                                                                                                                                                                                                                                        VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V-----IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 KE---NGQD----TDPQDESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-- 492
                                                                                                                                                                                                                                                                                         47 --TLNNVKVRDRYKYVLD-DASEIPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKKE- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                               1 MTFAYKIDGNEVI----FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTI-- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 APTDGNVD----YGYLLDGDETPLPDPRTRRQPDGVHALSRTFDPSAYSWQDDAWGGREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNF-----VVYIQNHDQVGNRGKG
                                                                                                                                                          63;
                                                                                                              Length 598;
                                                                                                                                                        92; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| | | | : : :|| || 529 GFEDTQVAFDEDARWLRFRRGGVQVLLNFSEQPVSLDGAGTALL 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 --- DRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLL 533
                                                                                                              DB 2;
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419 Seventh Street, N.W., Suite 300
                                                                                                                                   Pred. No. 1e-83;
                                                                                                          35.6%; Score 1060.5; 39.7%; Pred. No. 1e-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                        Matches 232; Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-605-501-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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APPLICANT: TSUGAKI, Keiji
APPLICANT: HATTONI, KEZUKO
APPLICANT: HATTONI, VEZUKO
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 FEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTI----TLNNVKVRDRYKYVLD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%; Score 1059; DB 1; Length 59 40.5%; Pred. No. 1.4e-83; 1.1ve 89; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                             COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                  5: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59834
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUBOTA=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB-1996
CLASSIFICATION: 435
                     RESULT 10
US-08-607-321-4
; Sequence 4, Application US/08607321
; Patent No. 5716813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFRENCE/DOCKET NUMBER: KUBG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 597 amino acids
amino acid
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Best Local Similarity 40.59
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                       Washington
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                                                                                              GENERAL INFORMATION:
APPLICANT: KUBOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-08-607-321-4
                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 VNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRRKTHGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAAL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 PETFRESKLDWAEAAEGDHARLLELYRSLTALRRSTPDLTKLGFEDTQVAFDEDARWLRF 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQD 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YDVWAPNAESVTL -- LAGGERYAMQRRAETGPEDAGWWTAAGAPTDGNVD----YGYLLD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 597;
               SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 1059; DB 1;
40.5%; Pred. No. 1.4e-83;
tive 89; Mismatches 190;
                                                     APPLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                      KUBOTA=5
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                                                                                      CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA: 1994
ATTORNEY APAGENT INFORMATION:
                                                                                                                                                                                                                                          NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: KUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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amino acid Y: linear

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TOPOLOGY:
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APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kasuko
APPLICANT: GUGTHORI, TSASUKO
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
CORRESPONDENCES: 18
CORRESPONDENCE ANDRESS:
ADDRESSEE: BROWDY AND NEIMARK
VNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSN 352
                                                                               FRRKTHGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAAL 404
                                                                                                                                                                                    405 YLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQD 457
                                                                                                                                                                                                                                                   ESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-----DRRVNVVNGENWLII 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,240
FLING DATE: 30-OCT-1997
CLASSIFICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: US 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: US 59840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                               508 KGREYFSLYVFSKSSIEVKYSGTLLL 533
                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08961240 Patent No. 5830715 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
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STATE: D.C.
COUNTRY: USA
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APPLICANT: TSUGAKI, Keiji
APPLICANT: HATTORI, Kasuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT, DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                     119 FEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEA 178
                                                                                                                                                                                                                                                                                                                                                                                           HKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 EYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIV-----IAESDLNDPRV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 -DASEIPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKKE--DLIIYEIHVGTFTPEGT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 VNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSN 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETFRRSKLDWAEAAEGDHARLLELYRSLTALRRSTPDLTKLGFEDTQVAFDEDARWLRF 545
                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 ESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC-----DRRVNVNGENWLII 507
                                                                                                                                                                                    14 FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTI----TLNNVKVRDRYKYVLD 62
                                                                                                                                                                                                             58;
                                                                                                 Length 597;
                                                                                                                                          Indels
                                                                                            ; Score 1059; DB 2;
; Pred. No. 1.4e-83;
89; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 KGREYFSLYVFSKSSIEVKYSGTLLL 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08605501
Patent No. 5834287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                              35.6%;
40.5%;
                                                                                              Query Match 35.6%
Best Local Similarity 40.5%
Matches 229; Conservative
, MOLECULE TYPE: protein US-08-961-240-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
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APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOSHIJUKI
TILE OF INVENTION: DNA BNCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| :| |||||| |: : :| :|||:||||||| : 68 PLPDPRTRRQPEGVHALSRTFDPGTLDAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 IRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AGKLDYLAGLGIDFIELLPVNAFNGTHNWGYDGVQWFAVHEGYGGPAAYQRFVDAAHAAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 FILWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%; Score 1025; DB 1; Length 589;
40.3%; Pred. No. 1.2e-80;
ive 80; Mismatches 197; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,646
FILING DATE: O'-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59834
FILING DATE: O'-MAR-1994
PRIOR APPLICATION NUMBER: JP 59840
FILING DATE: O'-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               : 419 Seventh Street, N.W., Suite Washington
    546 RRGGVQVLLNFSEQPVSLDGAGTALL 571
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                Sequence 2, Application US/08399646 Patent No. 5556781
                                                                                                                                                                                                                                                                                                               BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 amino acids
amino acid
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 589 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.3
Matches 229; Conservative
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY ANI
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                      GENERAL INFORMATION:
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COUNTRY:
                                                                              US-08-399-646-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TLTGPFTPMLLMGEEYGASTPWQFFTSHPEPELGKATAEGRIKEFERMGWDPAVVPDPQD 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKKGLGVILDVVYNHVGPEGNYMVKLCPYFSQKYKTPWGLTFNFDDAESDEVRKFILENV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 EYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIV-----IAESDLNDPRV 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 FILWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTI----TLNNVKVRDRYKYVLD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Mismatches 190; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1059; DB 2;
Pred. No. 1.4e-83;
                                                                                                        PURDATE APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION UNBER: UP 59834
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                   KUBOTA-5
                                                      UMBER: US/08/605,501
26-FEB-1996
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                                                                                                                                                                                      FILING DATE: 07-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 597 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-605-501-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                              CLASSIFICATION:
                                                                            FILING DATE:
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STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.
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COMPUTER: IBM PC compatible
                                                                                           Query Match
Best Local Similarity 40.39
Matches 229; Conservative
          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-607-321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
amino acid
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US-08-961-240-2
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Fatent No. 5716813
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HATTORI, Keiji
APPLICANT: HATTORI, Kazuko
TITLE OF INVENTION: BNZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: BNZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STRYE: D.C.
COUNTRY: USA
                                                                                                                                            THGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
                                                                                                                                                                                                            461
                                                                                                                                                                                                                             EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRK 356
                                                                                                PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTF
                                                                                                                                                                                                                                                                            NASKLSWK----IDEEIFSFYKILIKMRK-----ELSIACDRRVNVVNGENWLIIKGR
                                                                                                                                                                                                                                                                                                           482 TRSKLDWAEASAGDHARLLELYRSLITLRRSTPELARLGFA-DTAVEFDDDARWL----
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APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                         511 EYFS-----LYVFSKSSIEVKYSGTLLL 533
                                                                                                                                                                                                                                                                                                                                                                         536 RYWRGGVQVVLNFADRPISLDRPGTALL 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELECHHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAA.
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENOTH: 589 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20004
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Patent No. 5830715
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGINOTO, TOSSHAYUKi
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: BUZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             LGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 DVNGYGLAGQWSDDFHHAVHVNVSGETTGYYSDFDSLGALAKVLRDGFFHDGSYSSFRGR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
                                                                                                                                                                                                         66 EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                                                                                                        KEYNVDGFRLDAVHAIIDTSPKHILEE---IADVVHKYN---RIVIAESDLNDPRVVNPK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                       14 FTLWAPYOKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
                                                                                                                                                                                                                                    123 IRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                          462 NASKLSWK----IDEEIFSFYKILIKMRK-----ELSIACDRRVNVVNGENWLIIKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 THGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 TRSKLDWAEASAGDHARLLELYRSLITLRRSTPELARLGFA-DTAVEFDDDARWL----
                                                     62;
  Length 589;
34.4%; Score 1025; DB 1; Length 5 40.3%; Pred. No. 1.2e-80; Live 80; Mismatches 197; Indels
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357 THGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| : || : || 482 TRSKLDWAEASAGDHARLLELYRSLITLRRSTPELARLGFA-DTAVEFDDDARWL---- 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 IRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVNGYGLAGQWSDDFHHAVHVNVSGETTGYYSDFDSLGALAKVLRDGFFHDGSYSSFRGR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 NASKLSWK-----IDEEIFSFYKILIKMRK-----ELSIACDRRVNVVNGENWLIIKGR 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

34.4%; Score 1025; DB 2; Length 589;
Best Local Similarity 40.3%; Pred. No. 1.2e-80;
Matches 229; Conservative 80; Mismatches 197; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PLINGE OF THE STATE OF 
                                                                                                                                                                                                            CLASSIFLATION: 43.2
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/399,646
FILING DATE: U7-MAR-1994
APPLICATION NUMBER: UF 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUBOTA=5
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: KUT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248633
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-961-240-2
                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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511 EYFS----LYVFSKSSIEVKYSGTLLL 533

16;

Db 536 RYWRGGVQVVLNFADRPISLDRPGTALL 563

Search completed: July 15, 2002, 12:18:04 Job time: 96 sec

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July 15, 2002, 12:16:28 ; Search time 32.43 Seconds (without alignments) 1656.304 Million cell updates/sec
                                                                                                                                                                           US-09-298-924-6
2978
1 MIFAYKIDGNEVIFTLWAPY.....PQHIEEGKYEFDKGFALYKL
version 4.5 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Gaps

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Length 558; Indels

Score 2973; DB 2; Pred. No. 1.1e-185; 0; Mismatches 0;

tch 99.8%; Sc al Similarity 100.0%; P 558; Conservative 0;

Query Match Best Local Similarity Matches 558; Conserv

61 DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG 120

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62 DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG 121

122 VIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKK 181

242 IKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGY

182 GLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYW 241

301 300

;		dP			SUMMARIES	
Result No.	Score	Query Match	Length	DB	OI.	Description
1	2973	99.8	558	2	JC5135	alpha-amylase (EC
7	2467	82.8		~	573087	е
٣	1748.5	58.7		7	JC5132	o
₹	1288.5	43.3	620	7	AH1827	alpha-amylase [imp
2	1060.5	35.6	298	~	865770	Ϊ,
9	1025	34.4	296	7	JC4697	trehalose trehaloh
7	1024.5	34.4	575	~	JC7727	malto-oligosyltreh
80	997.5	33,5	580	7	G70763	probable maltoolig
6	978.5	32.9		~	AI0673	probable hydrolase
10	905.5	30.4		~	H75516	
11	881.5	29.6		7	G83375	qlycosyl
12	876.5	29.4		7	D96001	
13	860.5	28.9		~	AG3194	>
14	524.5	17.6		7	S19134	probable alpha-qlu
15	524.5	17.6		7	AH1915	hypothetical prote
16	391	13.1		7	B56639	7
17	374.5	12.6		Н	S40048	1,4-alpha-glucan b
18	374.5	12.6		7	S18599	1,4-alpha-qlucan b
19	365	12.3		7	E95031	alkaline amylopull
50	364	12.2		~	G97902	alpha-amylase (EC
21	361	12.1		7	D70363	1,4-alpha-glucan b
22	349.5	11.7	783	7	B84823	probable isoamylas
23	348.5	11.7	999	7	E71565	
24	347.5	11.7	764	7	AG1895	a
25	345.5	٠	422	7	S31839	1,4-alpha-qlucan b
36			664	~	B86539	qlycogen hydrolase
27	345.5	11.6	664	~	B72084	
28	345.5	11.6	999	7	G81717	
29	345.5	11.6	707	7	S77094	_

1,4-alpha-glucan b glycogen operon pr 1,4-alpha-glucan b probable isoamylas isoamylase-like pr 1,4-alpha-glucan b alkaline amylopull pullulanase amyX [glycogen operon pr hypothetical prote trehalose-6-phosph probable isoamylas probable branching 1,4-alpha-glucan b glycogen branching probable glycogen	RESULT 1 JUC5135 alpha-amylase (EC 3.2.1.1) - Sulfolobus solfataricus Cispecies: Sulfolobus solfataricus Cispecies: Sulfolobus solfataricus Cispecies: Sulfolobus solfataricus Cibate: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 CiAccession: JC5135 Rix Robayashi, X.; Kato, M.; Miura, Y.; Kettoku, M.; Komeda, T.; Iwamatsu, A. Biosci. Biotechnol. Biochem. 60, 1882-1885, 1996 A;Title: Gene cloning and expression of new trehalose-producing enzymes from the hype A;Reference number: JC5134; MUID:97141610 A;Reference number: JC5134; MUID:97141610 A;Reference number: JC5134; MUID:97141610 A;Relecule type: DNA A;Residues: 1-558 excma A;Relecule type: DNA A;Residues: 1-558 excma A;Cross-references: DDBJ:D64130; NID:9987702; PIDN:BAA11010.1; PID:91838936 A;Experimental source: strain KM1 C;Comment: This enzyme hydrolyzes starch alpha-1,4 linkage adjacent to the alpha-1,1 C;Superfamily: trehalose trehalohydrolase
S34218 S73088 I 164118 H 64118 H 7569 A 84112 B 7569 C 6223 I 149679 F 98228 A H 3057 A H 3057	ALIG Sulfolobus : ricus ricus Lrevision 2 ura, Y.; Ke 60, 1882-18 ression of UID: 9714161 UID: 9714161 Xzes starch Alohydrolass
нанавававававава	Sulfrictura, rrack tress of KMJ KMJ KMJ colass
741 718 730 703 704 1072 710 720 720 735 818 818 735 735 735 735 735 735 735 735 735 735	1.1) - solfata equence M.; Mi
11111111111111111111111111111111111111	3C 3.2. (1) as in the control of the
34. 33.34. 33.54. 33.64. 33.65. 33.65. 33.65. 33.65. 33.65. 33.65. 33.65. 35.65. 36.65	1 ylase ([3: Sulf, 3: Sulf, 3: Jan ion: JC, shl, K., shl, K., shl, K., conce num ion: JC,
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 JC5135 alpha-amylase (EC 3.2.1.1) - Sulfolobus solfat C; Species: Sulfolobus solfataricus C; Date: 31-Jan-1997 #sequence_revision 27-Feb-C; Accession: JC5135 R; Kobbyashi, K.; Kato, M.; Miura, Y.; Kettoku, Biosci. Biotechnol. Biochem. 60, 1882-1885, 19 A; Title: Gene cloning and expression of new tr A; Reference number: JC5134; MUID: 97141610 A; Accession: JC5135 A; Accession: JC5135 A; Molecule type: DNA A; Residues: 1-558 < (ROB) A; Cross-references: DDBJ: D64130; NID: 9987702; A; Experimental source: strain KMI C; Comment: This enzyme hydrolyzes starch alpha C; Superfamily: trehalobydrolase C; Keywords: glycosidase; hydrolase

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archaea

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hyperthermophilic
                                                                                                                                                                                 Wilternate names: glyogenase.
C;Species: Sulfolobus acidocaldarius
C;Species: Sulfolobus acidocaldarius
C;Species: Sulfolobus acidocaldarius
C;Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C;Accession: JC5132
R;Kobbyashi, K.; Kato, M.; Miura, Y.; Kettoku, M.; Komeda, T.; Iwamatsu, A. Biosci. Biotechnol. Biochem. 60, 1720-1723, 1996
A;Title: Gene analysis of trehalose-producing enzymes from hyperthermophilic A;Reference number: JC5131; MJID:97141330
A;Accession: JC5132
A;Acc
                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-556 <KOB>
A; Cross-references: DDBJ:D64131; NID:9987704; PIDN:BAA11011.1; PID:9987705
A; Cross-references: strain ATCC33909
C; Comment: This enzyme hydrolyzes glycosyltrehalose to liberate trehalose.
C; Superfamily: trehalose trehalohydrolase
C; Keywords: glycosidase; hydrolase
359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQ
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                                                                                                                                                                      alpha-amylase (EC 3.2.1.1) - Sulfolobus acidocaldarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.7%; Score 1748.5; DB 2 58.9%; Pred. No. 4.5e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 KLKKDELIKVNRGVGVYQL 555
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                                                                     FPSQITESKYELDKGFALYKL
                                                  FPQHIEEGKYEFDKGFALYKL
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Best Local Similarity
Matches 329; Conserv
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79.7%; Pred. No. 8.6e-153;
11ve 63; Mismatches 49;
                                                                                                                                                                   542 HIEEGKYEFDKGFALYKL 559
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Best Local 9
Matches 447
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C;Species: Arthrobacter sp.
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                                                                                                                  C; Species: Anabaena sp.
A; Mote: All B27
C; Accession: AH1827
C; Accession: AH1827
Nakacaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Triquchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sp.
NA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807
A; Mulb:21595285; PMID:11759840
A; Accession: AH1827
A; Molecule type: DNA
A; Residues: 1-620 (KGR>
A; Molecule type: DNA
A; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
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                                                                                               [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.3%; Score 1288.5; DB 2; Best Local Similarity 44.0%; Pred. No. 4.2e-76; Matches 255; Conservative 100; Mismatches 178;
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Superfamily: trehalose trehalohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain PCC 7120
C, Genetics:
A, Gene: 110168
C, Superfamily: trehalose trehalohydrola
                                                                                                  alpha-amylase
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maltooligosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)

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C;Species: Rhizoblum sp.
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C;Dates: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C;Accession: 104697
R;Marnta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto, T.; Kurimoto, M.
Biosci. Biotechnol. Biochem. 60, 717-720, 1996
A;Title: Cloning and sequencing of trehalose biosynthesis genes from Rhizoblum sp. M-A;Reference number: JC4696; MUID: 96219094
A;Accession: JC4697
A;Molecule type: DNA
A; Variety: strain 036
C; Date: 28-0ct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Date: 28-0ct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: S65770
Biochim: Biophys. Acta 1289, 10-13, 1996
A; Title: Cloning and sequencing of trehalose biosynthesis genes from Arthrobacter: A; Reference number: S65769; MUID:96195835
A; Reference number: S65770
A; Reference number: S65770
A; Releas: 1-598 < WAR>
A; Wolecule type: DAA
A; Residues: 1-598 < WAR>
A; Residues: 1-598 < WAR>
C; Superfamily: trehalose trehalohydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 NFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 DIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNF------VVYIQNHDQVGNRGKG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRK 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 ALAKVLRDGFFHDGSYSSFRERHHGRPI-----NFSAVHPAALVVCSQNHDQIGNRATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 --TLNNVKVRDRYKYVLD-DASEIPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKKE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.6%; Score 1060.5; DB 2; 39.7%; Pred. No. 2.7e-61; ive 92; Mismatches 197;
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Best Local Similarity
Matches 232; Conserv
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Matches 215;
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A;Gene: glgZ
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A; Residues: 1-596 <MAR>
A; Residues: 1-596 <MAR>
A; Cross references: DDBJ:D78001; NID:g1040695; PIDN:BAA11187.1; PID:g1040697
C; Comment: This enzyme belongs to the alpha-amylase family. It hydrolyzes the products oligosyl group and trehalose.
C; Genetics:
A; Gene: MTHase
C; Superfamily: trehalose trehalohydrolase
C; Superfamily: trehalose trehalohydrolase
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maito-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) - Arthrobacter ramosus C; Species: Arthrobacter ramosus C; Date: 14 - Dec.2001 #cequence_revision 14-Dec.2001 #ccasion: JC7727; PC7175 PC7176 PC71776 PC7177 PC71776 PC7177 PC717 PC7177 PC7177 PC7177 PC7177 PC717 PC7177 PC7177 PC7177 PC7177 PC7177 PC7177 PC7177 PC7177 PC7177 PC717 PC7177 PC7177 PC717 PC717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THGEPVGELDGCNF-----VVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDL---IIYEIHVGTFTPEGTFEGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 IRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 AGKLDYLAGLGIDFIELLPVNAFNGTHNWGYDGVQWFAVHEGYGGPAAYQRFVDAAHAAG 194
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              14 FILWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
                                                                                                                                                                                                                                                                                                                                                                               KEYNVDGFRLDAVHAIIDTSPKHILEE---IADVVHKYN---RIVIAESDLNDPRVVNPK
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                                                                                                                                                                                                                                                   Length 596;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                              34.4%; Score 1025; DB 2; 140.3%; Pred. No. 5.5e-59; ive 80; Mismatches 197;
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Best Local Si
Matches 2299
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Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Accession: G70763
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-580 <COL>
A;Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98329.1; PID:g14034 A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (strain
                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable maltooligosyltrehalose trehalohydrolase - Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LIIYEIHVGTFTPEGTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPRSLRQPRGVH-----ELGREFDPARYAWGDDGWRGRDLTGAVIYELHVGTFTPEGTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA----DVVHKYNR--IVIAESDLNDPRVV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRKTHGEPVG-ELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIFMGEEYGEENPFYFFSDFSDFSKLIQGVREGRKKE---NGQD----TDPQDESTFNASK 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 FILWAPYQKSVKLKVLEKGLYE--MERDEKGYFTITL---NNVKVRDRYKYVLDDASEIP 68
                                                                                                                                                                                                                                                                                                                                                                                                      | :||| | | | |::| | : ||| |::|
FPVWAPQAAQVIL-VVGQGRAELPITRDENGWWALQQPWDGGPDLVD-YGYLVDGKGPFA 62
C;Comment: This enzyme is involved in producing trehalose from glycogen C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 KKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 NPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSWKIDEE-----IFSFYKILIKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSK
                                                                                                                                                                                                      5; DB 2; Length 575;
6e-59;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                               189;
                                                                                                                                                                                                                                      34.4%; Score 1024.5;
ilarity 39.4%; Pred. No. 5.6e
Conservative 90; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPASRYQPEGVHGPSQIIQESKEFNNETFLKKED-
                                                                                                               trehalohydrolase
hydrolase
                                                                               A,Gene: treZ
C,Superfamily: trehalose
C,Keywords: glycosidase;
                                                                                                                                                                                                                                                                      Similarity
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probable maltooligosyltrehalose trehalohydrolase - Deinococcus radiodurans (strain RJ C;Species: Deinococcus radiodurans C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: H75516 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C., Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aritle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUD:20036896
A; Reference number: H75316
A; Status: pre-liminary
A; Molecule type: DNA
A; Residues: 1-600 < WHI>
A; Residues: 1-600 < WHI>
A; Residues: GB: AE001905; GB: AE000513; NID: 96458144; PIDN: AAF10042.1; PID: 9645
A; Cross references: Strain R1
C; Genetics: C; Genetics: Strain R1
                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                              411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVILDVVYNHVGPEGNYMVKLGP-YFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWI 242
                                                                                                                                                                                                                                                                                                                                                                                      KEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHK---YNRIVIAESDLNDPRVVNPKEKC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYN--IDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDD--IVKSYKDVFVYDGKYSNFRR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE----NGQDT-DPQDESTFNASKL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEIPDPASRYQPEGVHGPSQIIQESKEFNNETF------LKKEDLIIYEIHVGTFTP 115
                                                                                                                                       67 IPDPASRYQPEGVHGPSQIIQESKEFNNETFLKK---EDLIIYEIHVGTFTPEGTFEGVI 123
                                                                                                                                                                                                                          124 RKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                    15 IAADVVRFRLWATGQQKVMLRLAGKD-QEMQASGDGWFTLDVSGVTPGTEXNFVLSDGMV 73
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                               FRLWTSTARTVAVRVNGTEHVMTSLGGGIYELELP------VGPGARYLEVLDGV
                                                           IDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTHGEPVGELD----GCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTLWAPYQKSVKLKV------LEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDA
                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600;
                     Indels
ed. No. 5.7e-56;
Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%; Score 905.5; DB 2
38.7%; Pred. No. 3.2e-51;
  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: DRO464
A;Map position: 1
C;Superfamily: trehalose trehalohydrolase
                16;
  43.38;
                209; Conservative
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  Similarity
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205; Conserv
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NWK 488
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Best Local
Matches 20
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Matches
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Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A;Reference number: AB0502; PMID:11677608
                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-594 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01762.1; PID:916502610; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYN 246
                                                                                                                                                                                                                                                                                                                                                                                                       PV -- GELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 RYQPEGVHGPSQIIQESKEF---NNET---FLKKEDLIIYEİHVGTFTPEGTFEGVIRKL 126
                                                                                                                                                                                                                                               DYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVI 186
                                                                                                                                                                                                                                                                                                                             VDGFRLDAVHAIIDTSPKHILEEIADVVHKYN-----RIVIAESDLNDPRVVNPKEKCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYGEENPFYFFSDFSDSKLIQGVREGRKKENGQD-----TDPQDESTFNASKLSWK-- 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---IDEEIFSFYKILIKMRKELSIACD-----RRVNVVNGENWLIIKGREYFSLYVFSKS 521
                                                                                                   Gaps
                                                                                                                                       14 FTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL-DDASEIPDPAS 72
                                                                                                                                                                               FRVMAPKPALVRLDV-NGAVHAMTRSADGWWHTTV-AAPADARYGYLLDDDPTVLPDPRS 61
                                                                                                 35;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length
                                                         Score 997.5; DB 2;
Pred. No. 3.2e-57;
                                                                                               91; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB
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C; Superfamily: trehalose trehalohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: trehalose trehalohydrolase
                                                       33.5%;
38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%;
                                                                                               Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | || ||:|:
541 PTCVPVSGELVLA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIEVKYSGTLLLS 534
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AI0673
A; Status: preliminary
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                                                           Query Match
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probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - Sinorhizobium m C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Special C; Marian Second C; Species Second C; Sp
                                                                                                                                                                                                          403
                                                                                                                                                                                                                                                 401
    DSAHGMGLMVFVDVIYNHFGPDGNYLAQYAAAFFRDDRQTPWGQAIDF---RRGEVREFF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 IPDPASRYQPEGVHGPSQIIQESK-EFNNETFLKK--EDLIIYEIHVGTFTPEGTFEGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                LYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE
                                                                                                                         SDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGN-LDDIVKSYKDV
                                                                                                                                                                                                          FVYDGKYSNFRKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                        453 -TDPQDESTFNASK-----LSWKIDEEIFSFYKILIKMRKELSI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: plasmid
C;Superfamily: trehalose trehalohydrolase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 876.5; DB 2
35.3%; Pred. No. 2.5e-49;
iive 99; Mismatches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 --- ACDRRVNVVNGENWLI 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: glgB2; SMb21447
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137		Qy 182 GLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYW 241
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Db 197 TVLLDVVYNHFGPEGNYLSRYASRFFNKDRPTPWGASIAFEEEAVRRYFIENALYWL	VRRYFIENALYWL 253	Qy 242 IKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPK 296
243	ENDPRVVNPKEKC 299	Db 247 LETYRFDGLRIDAADHLAGGDGEVDFLIEMAREVKRTIRNRHVHLVIEDARNAASPMTPM 306
Db 254 GHFRFDGLRLDATEQIRDTTKPHFLVALEHEVREAFAERQIHLVLEDAHRRRSLLQRDAS	AHRRESLLORDAS 313	QY 297 EKCGYNIDAQWVDDFHHSIHAYLTGERQGYTDFGNLDDIVKSYKDVFVYDGKYSNFR 354
300	VEVYDGKYSNFR- 354	VIHVATTNEEGGIYEDFASRPY
314		355 R-KTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPM
		NFAASGEPSGHLPPHRFVNFLHNHDQAGNRLRGERLRALIPPPLFGTLEAILLLCPQTPL
374		414 IFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKK-ENGQDTDPQDESTFN
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DD 487 FAGSKLRWNRATSPAGERHLAYVRDLAVIRQRHIVPLIAGTAVPDGRAYETKDGIIAVDW	AYETKDGIIAVDW 546	QY 505 LIIKGREYFSLYVESKSSIEVKYSGTLLLSSNNSFPQHIEEGKYE-FDKGFALY 557
OY 487 ELSIAC-DRRVNVVNGENWL-IIKGREYFSLYVFSKSSIEVKYSGTL 53		Db 544 HFKAGRLEMRANL-SENMCELPAVKGEILHRNGSVGNTRYEQYAAQFAIY 592
RGQP1FTSETSSVETVIGSEL	056	RESULT 14
RESULT 13		S19134 probable alpha-glucanotransferase - Anabaena variabilis
A03124 alpha-amylase Atu5284 [imported] - Agrobacterium tumefaciens (strain C58, D C:Species: Agrobacterium tumefaciens	ens (strain C58, Dupont) plasmi	C:>Pecies: Anabaena Variablils C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000 C:Accession: G19134
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_charcassion. AG3194	change 01-Feb-2002	C. NOCCESSION: 317134 R. SELON N. 19 166-170 1000
, R.; Monks, D.; Chen, L. Guenthner, D.; Kutyavin,	.; Wood, G.E.; Chen, Y.; Woo, I , T.; Levv, R.; Li, M.; McClell	Figur Moi. Bloi. 16, 163-1/0, 1992. A;Title: Cloning of a low-temperature-induced gene lti2 from the cyanobacterium Anaba A;Reference number: S19133: MJD:92119230
		A; Accession: S19134 A; Status: preliminary
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, ster, E.W.	n, W.; Perry, M.; Gordon-Kamm,	A;Molecule type: DNA A;Residues: 1-552 <sat></sat>
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A:Reference number: AB2577; PMID:11743193 A:Accession: AG3194	acterium tumefaciens C58.	A;Cross-references: EMBL:X59279; NID:g39252; PIDN:CAA41970.1; PID:g39253 C;Superfamily: neopullulanase; alpha-amylase core homology
A; Status: preliminary A; Molecule type: DNA		
A; Residues: 1-595 < KUR> A; Residues: 1-595 < KUR> A; Cross: references: GB: AE008687; PIDN: AAL45973.1; PID: 917743726;	743726; GSPDB:GN00188	Similarity 28.0%; Pred. No. 1.7e-26; 8; Conservative 90; Mismatches 162;
Apartmental source: Strain C30 (Dupont) (Genetics:		QY 14 FILWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKKVLDDAS 65
A)Gene: Atu>284 A;Genome: plasmid (f.Ginorfamily: trobaloes trobalokudvolese		Db 7 FTLFAPYNKGAALIASFSDWQEIPWKKGDDGYFRTTVELEDGTYQYKFRVQTRSWFF 63
		Qy 66EIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEI 108
atch 28.9%; Score 860.5; I cal Similarity 34.7%; Pred. No. 2.7e-	ngth 595;	Db 64 EEDQWVDVTDPYATDIDES-SGKDNSIARIKDGEKIVDTYVWQHDDKPLPADHELVIYEL 122
vative 89	dels 53; Gaps 16;	QY 109 HVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDMGYDGVYLYAV 161
* (123 HVGDFSGGGDDFYAKGKYKHVIEKLDYDCELGINAIELLFVKEYFGDYSWGYNFKYFFAY
DD 12 AQRHQSGDTDFSIMAPASATVKL-WLNDABEFDMHTAGDGWHDIT-KPALPGDRYGFVLAD QY 64 ASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG	ALPGDRYGEVLAD 69 HVGTFTPEGTFEG 121	QY 162 QNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNY-MVKLGPYFSQKYKTPWG 217 :: : :: : : Db 183 ESSYGSTADLKKLVDECHQRGIRIIMDGIYNHSEASSPLTQIDHDYWYHHEPRDFDNNWG 242
DD 70 RTRVADPASNRQQEGPRGPSLIVNHDFAWKNPWWKGRPWHEAVVYELHIGTFTPEGTFAA	HIGTETPEGTEAA 129	Qy 218 LTENFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEE 269
Db 130 AAEKLEYLADVGITTIELMPLATFAGSRGWGYDGVLQFSPQRDYGTPDELKAFIDQAHGH	DELKAFIDQAHGH 189	OY 270 IADVVHKYNRIVIAESDLNDPRVVNPKEKGGYNIDAQWVDDFHHSIHAYLIGERQGY 326

Oy 438 IQC Db 430 Search comple Job time: 135	
Db 303 TAGAKPFYNVAEHIPETTSITNLDGPMDGCWHDSFYHTIKAHICGDT 349 Qy 327 YTDFGNLDDIVKSYKDVFVYDGKYSNFRKTHGEPVGELDGCNFVYYIQNHDQV 380 L	PRESENT: 15 AN1915 AN19

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SUMMARIES

	Description	Q44316 arthrobacte	Q53238 rhizobium s	Q9ajn6 arthrobacte	Q10769 mycobacteri				P30538 bacillus st	P45177 haemophilus	P52980 streptomyce		P16954 synechococc		P30539 butyrivibri				'n	P14899 dictyoglomu	-	10	P29094 bacillus th		-		escheric	P30924 solanum tub	_	Q04446 homo sapien		9	047 zea mays	Q01401 oryza sativ
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Maruta K., Hattori K., Nakada T., Kubota M., Sugimoto T., Kurimoto M.;
"Cloning and sequencing of trehalose biosynthesis genes from Rhizobium
                                                                                                                                                                 VQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | || | ::::::|| 59 APTDGNVD----YGYLLDGDETPLPDPRTRRQPDGVHALSRTFDPSAYSWQDDAWQGREL 114
                                                                     -DLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYA 160
                                                                                                  NFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRI 280
                                                                                                                                                                                                                                                                                                                                                                             DIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNF------VVYIQNHDQVGNRGKG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492
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                                                                                                                                                                                                                                                                                  V-----IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLD 334
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CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic
linkage in 4-alpha-D-{(1->4)-alpha-D-glucanosyl}(n) trehalose
yield trehalose and alpha-(1->4)-D-glucan.
PATHWAY: Trehalose biosynthesis.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 KE---NGQD----TDPQDESTFNASKLSWKIDEE----IFSFYKILIKMRKELSIAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) (MTHase)
alpha-D-{(1->4)-alpha-D-glucano|trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium sp. (strain M-11).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- DRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLL 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 EKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRK 356
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                                                                                                                                                                                                                                                                                                        75 PLPDPRTRRQPEGVHALSRTFDPGAHRWQDAGWQGRELQGSVIYELHIGTFTPEGTLDAA 134
                                                                                                                                                                       Gaps
                                                                                                                                                                                                       14 FTLWAPYQKSVKLKVLEKG-LYEMER-----DEKGYFTITLNNVKVRDRYKYVLD-DAS 65
                                                                                                                                                                                                                                      17 FDIWAPEAGTVTL -- LAGGERYEMGRRPGNGPADEGWWTAADAPTGADVDYGYLLDGDEI 74
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                                                                                                                                                                       62;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe H., Yamashita H., Kubota M.,
                                                                                                                                   Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose translohydrolase (EC 3.2.1.141) (MTI
alpha-D-{(1->4)-alpha-D-glucano}trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase).
                                                                                  73EA80AE0534DDCD CRC64;
                                                                                                                                     34.4%; Score 1025; DB 1; 40.3%; Pred. No. 8.4e-60;
                                                                                                                                                   Pred. No. 8.4e-
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                                                                  BY SIMILARITY
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InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase.
ACT_SITE 265 265 BY SIMI
SEQUENCE 596 AA; 65262 MW. 77222
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                                                                                                                                                                     80;
                                                                                                                                                                       Conservative
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Fukuda S., Kurimoto
                                                                                                                                                     Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                       Best Local Sim
Matches 229;
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                                                                                                                                     Query Match
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.)
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.
                                                                                                                                                                                                                                                 MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Gordon S.V., Elglmeler K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd SHornsby T., Jagels K., Krogh A., MoLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) (MTHase)
                                                                                  alpha-D-{(1->4)-alpha-D-glucano}trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase).
TREZ OR RV1562C OR MT1613 OR MTCY48.03.
                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 393:537-544(1998).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID-1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGR; MT1613; -
                                                                                                                                                                                                                                     STRAIN=H37RV
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                  . There are no restrictions on its long as its content is in no way moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 YWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA----DVVHKYNR--IVIAESDLNDPRVV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 YWLRDMHADGLRLDAVHALRDARALHLLEELAARVDELAGELGRPLTLIAESDLNDPKLI 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 RSRAAHGYGLDAQWDDDVHHAVHANVTGETVGYYADFGGLGALVKVFQRGWFHDGTWSSF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 RRKTHGEPVG-ELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSWKIDEE-----IFSFYKILIKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSK 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 FTLWAPYQKSVKLKVLEKGLYE--MERDEKGYFTITL---NNVKVRDRYKYVLDDASEIP 68
"Trehalose producing operon treYZ from Arthrobacter ramosus S34.";
            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic linkage in 4-alpha-D-{(1->4)-alpha-D-glucanosyl}(n) trehalose yield trehalose and alpha-(1->4)-D-glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Trehalose biosynthesis.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                         34.4%; Score 1024.5; DB 1; Length 575; 39.4%; Pred. No. 8.6e-60; Live 90; Mismatches 189; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                    284A3F20207E228B CRC64;
                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                   entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                      InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                   EMBL; AB045141; BAB40766.1; -.
                                                                                                                                                                                                                                                                                                                                                                       63079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 39.49
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                        Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                       575 AA;
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S.L.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic linkage in 4-alpha-D-{(1->4)-alpha-D-glucanosyl}(n) trehalose to yield trehalose and alpha-(1->4)-D-glucan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Trehalose biosynthesis.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
506190468F44B862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.5%; Score 997.5; DB 1
38.3%; Pred. No. 5.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Glycosidase; Complete proteome
                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE007027; AAK45880.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist; Rv1562c; -.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64076 MW;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z74020; CAA98329.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212;
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Matches
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580 AA.

PRT;

STANDARD;

TREZ_MYCTU

TREZ_MYCTU

RESULT ΩI

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                                                                                                            300
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                                                                300
                                                                                                                                                                                                   480
        RYQPEGVHGPSQIIQESKEF -- - NNET -- - FLKKEDLIIYEIHVGTFTPEGTFEGVIRKL 126
                     ARQPDGVHARSQRWEPPGQFGAARTDTGWPGRSVEGAVIXELHIGTFTTAGTFDAAIEKL 121
                                                   DYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ц
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Brevibacteriaceae; Brevibacterium.
NCBI_TaxID=1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYN
                                                                                                                                                       361 PV--GELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGE
                                                                                                                                            247 VDGFRLDAVHAIIDTSPKHILEEIADVVHKYN-----RIVIAESDLNDPRVVNPKEKCG
                                                                                                                                                                                        YNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGE
                                                                                                                                                                                                                                                                                 EYGEENPFYFFSDFSDSKLIQGVREGRKKENGQD-----TDPQDESTFNASKLSWK--
                                                                                                                                                                                                                                                                                              |:| :|| || : :| || || : || EWGASSPFQFFCSHPEPELAHSTVAGRKEEFAEHGWAADDIPDPQDPQTFQRCKLNWAEA
                                                                                                                                                                                                                                                                                                                            ---IDEEIFSFYKILIKMRKELSIACD-----RRVNVVNGENWLIIKGREYFSLYVFSKS
                                                                                                                                                                                                                                                                                                                                                  481 GSGEHARLHRFYRDLIALRHNEADLADPWLDHLMVDYDEQQRWVVMRRGQLMIACNLGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- PATHWAY: Trehalose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) (MTHase)
alpha-D-[(1->4)-alpha-D-glucano|trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brevibacterium helvolum.
                                                                                                                                                                                                                                                                                                                                                                                             541 PTCVPVSGELVLA 553
                                                                                                                                                                                                                                                                                                                                                                        SIEVKYSGTLLLS 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 11822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TREZ_BREHE
O52520;
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
TREZ_BREHE
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                                                                         122
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                                                                                                                                                                                                                                                                                                                                                                                                               412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRHHGRPINPSLANPAALVVCNQNHDQIGNRATGDRLSQSLSYGQLAVAAVLTLTSPFTP 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545
                                                                                                                                                                                                                                                                                                                       PDPASRYQPEGVHGPSQII-----QESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFE 120
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                FTLWAPYQKSVKLKVLEKGLYEMERDE-----KGYFTITLNNVKVRDRYKYVLD-DASEI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                      WIKEYNVDGFRLDAVHAIIDTSPKHILEE---IADVVHKYN---RIVIAESDLNDPRVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKTHGEPVGE--LDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE---NGQD----TDPQDESTFNASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 LSWK-----IDEEIFSFYKILIKMRKELSIACD-----RRVNVVNGENWLIIKGREYFSL
                                                                                                                                                                                                             44;
                                                                                                                                                                            Length 589;
                                                                                                                                                                                                               Indels
                                                                                                     ' SIMILARITY.
C282314B6E9BA029 CRC64;
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G
                                                                                                                                                                          Score 965; DB 1; L. Pred. No. 6.9e-56; 3; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kiel J.A.K.W., Boels J.M., Beldman G., Venema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          666 AA
send an email to license@isb-sib.ch)
                                          InterPro; IPR000461; Alpha_amylase. Pfam; PF00128; alpha-amylase; 1. Hydrolase; Glycosidase. ACT_STIE: 258 SEQUENCE 589 AA; 64217 MW: C287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=93208370; Pubmed=1296817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 VNLSDAKVRLDDAAGDLLLATDEGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 YVFSKSSIEV-KYSGTLLLSSNNSFP
                                                                                                                                                                                                               88;
                                                                                                     258 258 E
589 AA; 64217 MW;
                                                                                                                                                                            32.4%;
38.5%;
                                   EMBL; AF039919; AAB95369.1;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus caldolyticus.
Bacteria; Firmicutes;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                              Best Local Sim
Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGB_BACCL
                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
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                                                                                                                                                                                                                                                  nt is in no way and for commercial
                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NETFLKK------EDLIIYEIHVGTF--TPEGTF----EGVIRKLDYLKDLGITAIEI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNYMVKLGP---YFSQKYKT--PWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAVHAII-----DTSPKHILEEIADVVHKY--NRIVIAESDLNDPRVVNPKEKCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 DSPWQRKKRRKRIYDQPMVIYELHFGSWKKKPDGRFYTYREMADELIPYVLERGFTHIEL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GPE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 PVGELDGCNFVVYIQN-----HDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYI--- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- NOVSFSLLYAYSENFILPFSHDEVVH-GKKSLLNKMPGSYEEKF-AQLRLLYGYMMAH 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 4EELDW 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202; Indels 170; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 KIDEEIFSFYKILIKMRKELSIACDRRVNVV-----NGENWLIIKGREYFSLYVFSKS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKGYFTITLNNVKVRDRYKY -- VLDDASEI -- PDPASRYQPEGVHGPSQIIQESK -- EFN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KVLEKGLYEMERD 39
     Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene from the thermophile Bacillus caldolyticus encodes
                                                                                                                                    SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAVANMLYWPNNDRLYENPYAVEFLRQLNEAVFAYDPNVWMIAEDSTDWPRVTAPTYDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 YNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 LGFNYKW---------NMGWMNDMLK-YMETPPHERKYAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSW
                                                                     glycogen.
PATHRAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
MISCELLANEOUS: OPTIMAL ACTIVITY AT APPROXIMATELY 39 DEGREES
                                                      σţ
                                                    -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 666; 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

1. 1F64C31495BB1B6E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 2.7e-
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AYKIDGNEVI------FTLWAPYQKSVKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 391;
                                                                                                                                                                                                                                                                                                                                                                                                                      Glycogen biosynthesis; Transferase;
ACT_SITE 309 309 BX SIMI
ACT_SITE 352 BY SIMI
ACT_SITE 420 BY SIMI
SEQUENCE 666 AA; 78096 MW; IF64C
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%;
                                                                                                                                                                                                                                                                                                                                    EMBL; 214057; CAA78440.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                  DNA Seq. 3:221-232(1992)
              thermolabile branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 155; Conserv
                                                                                                                        CELSIUS
 glgB
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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481 VLFD--FELHRKMDEYVKQL-IACYKRYKPFYELDHDPRGFEWIDVHNAEQ-SIFSFIRR 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region.",
microbiology 143:3431-3441(1997).

-!- FUNCTION: CATALYSES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC
LINKAGES IN GLYCOGEN BY SCISSION OF A 1,4-ALPHA-LINKED
OLIGOSACCHARIDE FROM GROWING ALPHA-1,4-GLUCAN CHAINS AND THE
SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF
ALPHA-1,4-GLUCAN CHAINS.
                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycogen.
PATHRAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON
SOURCES THAT ALLOW EFFICIENT SPORULATION.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                                                                                                           Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.; "Glycogen in Bacillus subtilis: molecular characterization of operon encoding enzymes involved in glycogen biosynthesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
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Y SIMILARITY.
Y SIMILARITY.
64B0A5553B6767BA CRC64;
                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                    627 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S36624; S36624.
Subtilist; BG10907; g1gB.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94195107; PubMed=8145641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98048467; PubMed=9387221;

    Microbiol. 11:203-218(1994).

                                                     G---KKEGDVLVIVCNFTNQAYDDYK
                                 SIEVKYSGTLLLSSNNSFPQHIEEGK
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EMBL; Z99119; CAB15076.1;
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                                                                                                                                                      STANDARD;
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P39118;
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SEQUENCE
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MEDLINE-92079888; PubMed=1745226;
Kiel J.A.K.W., Boelds J.M., Beldman G., Venema G.;
Molecular cloning and nucleotide sequence of the glycogen branching enzyme gene (glgB) from Bacillus stearothermophilus and expression in Escherichia coli and Bacillus subtilis.";
                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVGTFTPEGTFEGVIRK-----LDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQ 162
                                                                                                                                                                                                                                                                      273
                                                                                                                                                                                                                                                                                                   WGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAII---DTSPKHILEEIAD 272
                                                                                                                                                                                                                                                                                                                               331
                                                                                                                                                                                                                                                                                                                                                                                      332 FLKKLNOTMREAYPHVMMIAEDSTEWPQVTGAVEEGGLGFHYKW-------375
                                                                                                                                                                                                                                                                                                                                                                                                                                      423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527
                                                                                                                      ASEI-------PDPAS-RYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEI 108
                                                                                                                                                  97 NGEIRLKADPYAIYSEVRPNTASLTYDLEGYSWODOKWOKKOKAKT---LYEKPVFIYEL 153
                                                                                                                                                                                                                                                                                                                                                           273 VVHKYNR-----IVIAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGER 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQD------ESTFNASKLSW--- 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----FDEWKDTEQLDWFLDSFPMHQKASVFTQDLLRFYQKSKILYEHDHRAQSFEWIDV 523
                                 Gaps
                                                             FTLWAPYQKSVKLKVLEKGLYE------MER-DEKGYFTITLNNVKVRDRYKY-VLDD 63
                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                         SFGPPHDLMKFVDECHQQNIGVILDWVPGHFCKDAHGLYMFDGEPLYEYKEERDRENWL
                                                                                                                                                                                                                                                                                                                  154 HLGSWKKHSDGRHYSYKELSQTLIPYIKKHGFTHIELLPVYEHPYDRSWGYQGTGYYSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 NSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GPEGNYMVKLGPYFSQKYKTP----
                                                                                                                                                                                                                                                                                                                                                                                                                     QGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRTHGEPVGELDGCNFVVYIQ-----
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                                147;
    Length 627;
                                Indels
Score 374.5; DB 1;
Pred. No. 3e-17;
1; Mismatches 223;
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Bacteria, Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Geobacillus.
NCBI_TaxID=1422;
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   12.6%; Scc
23.1%; Pre
tive 94;
                                Conservative
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                Similarity
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P30538;
01-APR-1993 (
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNETFLKK------EDLIIYEIHVGTF--TPEGTF----EGVIRKLDYLKDLGITAIE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 IMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLGFNYKW------TYMETPPEHRKYVHN 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPVGELDGCNFVVYIQN-----HDQVGNRGKGERIIKLVDRESYKIAAAL---YLLS- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSW 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDAVHAII------DTSPKHILEEIADVVHKY--NRIVIAESDLNDPRVVNPKEKC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 VDAVANMLYWPNSDVLYKNTYAVEFLOKLNETVFAYDPNILMIAEDSTDWPRVTAPTYDG 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AYKIDGNEVI - - - - - FTLWAPYQKSVKL - - - - - - - - - KVLEKGLYEMERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 NDQTWRRKKQRKRIYDQPLFIYELHFGSWKKKEDGSFYTYQEMAEELIPYVLEHGFTHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGNYMVKLGPYF - - - - SQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFR
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                                                                                                  ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639;
                                              PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
MISCELLANBOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS
APPROXIMATELY 55 DEGREES CELSIUS.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
KNOWN AS THE ALPHA-AMYLASE FAMILY.
Mol. Gen. Genet. 230:136-144(1991).
                                                                                                                                                                                                                                                                                                                                                                                    Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY. F5BD4446B371E03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 374.5; DB 1;
Pred. No. 3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190;
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                               PIR; S18599; S18599.
InterPro: IPR000461; Alpha_amylase.
InterPro: IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; I.
Pfam; PF02922; isoamylase_N; I.
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                                    glycogen.
PATHWAY: '
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Best Local Simi
Matches 141;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P52980;
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95350630; PubMed-7542800; MEDLINE-95350630; PubMed-7542800; Plaischmann R.D. Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley K., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Ruhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDD-------ASE1-PDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLII 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || : | | | || | : | : | : | : | : | DGVSGVNFLWAPNARRVSI-VGDFNYWDGRRHPMRFHSKSGVWELFLPKASLGQLYKFE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 340; DB 1; Length 730;
ilarity 24.1%; Pred. No. 6.5e-15;
Conservative 101; Mismatches 214; Indels 158; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DG-NEVIFTLWAPYQKSVKLKVLEKGLYEMER-----DEKGYFTITLNNVKVRDRYKYV 60
                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycogen biosynthesis; Transferase; Glycosyltransferase;
Complete proteome.
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( SIMILARITY.
589575317F53769A CRC64;
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                                                                                               730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000461; Alpha_amylase.
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Pfam; PF02922; isoamylase_N; 1.
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                                                                                               STANDARD;
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Best Local Simi
Matches 150;
                                                                                               GLGB_HAEIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           ---DISPKHILEEIADVVH------KYNRIVIAESDLNDPRVVNPKEKCGYNIDAQWV 308
                                                                                                                                                                                                                                                                                                                                                                                                                   423 IPNQYGGRENLEAIEFLKHTNWKIHSEMAGAISIAEESTSFAGVTHPSENGGLGFNFKWN 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homerova D., Kormanec J.; "Cloning of the putative glycogen branching enzyme gene, glgB, from
                                                                                                                                                   DDFHHSIHAYLTGERQGYYTDFGNLDDIVKSY - - - KDVFVYDGKYSNFRRKTHGEPVGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 A------DWFLLDENIGGGWH
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Bacteria, Firmicutes; Actinobacteria; Actinomycetales; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1894;
                                                                                                                   YAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIA--AALYLLS---PYIPMIFMGEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSW-KIDEEI-FSFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 KILIKMRKELSIACDRR-----VNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLL
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-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                       ----WG-LTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAII-----
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Biochim. Biophys. Acta 1200:334-336(1994).
-!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
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STRAIN=CCM 3239 / ATCC 10762;
MEDLINE=94347823; Pubmed=8068720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 LSSNNSFPQHIEE-----GKYE 549
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EI-PDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLI-----IYEIHVGTFTPE 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTP-----WGLTFNFDDAESD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DALHRAGIGVIVDWVPAHFPRDDWALAEFDGRPLYEHODPRRAAHPDWG-TLEFDYGRK- 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVRKFILENVEYWIKEYNVDGFRLDAVHAII------DTSPK------HILE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EI-ADVVHKYNRIV-IAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGE---R 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 KYHHHDMTFG----MVXARSE-------558 KYHHHDMTFG----MVXLPI-SHDEVV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 NRGKGERIIKL-----VDRESYKIAAALYLLSPYIPMIFMGEEY--GEE-----NPFYFF 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 H-GKRSLVSKMPGDWWQQRATHRAYLGFMWAHPGKQLLFMGQEFAQGSEWSETYGPDWWV 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGYYTD--FGNLDDIVKSYKDVFVYDGKYSNFRKTHGEPVGELDGCNFVVYIQNHDQVG 381
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                     14 FTLWAPYQKSVKL----KVLEKGLYEMER-DEKGYFTITLNNVKVRDRYKYVL---DDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 LDSSYPAAGDH---LGVRSLVRDLN------RTYTASPALWERDSVPEGFAWVEADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 SDFS-----DSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWK--------
                                                                                                                                                                                                                      11.2%; Score 335; DB 1; Length 764; 24.2%; Pred. No. 1.5e-14; Live 90; Mismatches 197; Indels 130;
                          InterPro; IPR000461; Alpha_amylase.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR004193; isoamylase_N.
Pfam; PF02922; isoamylase_N.
Pfam; PF02922; isoamylase_N.
Glycogen blosynthesis; Transferase; Glycosyltransferase.
ACT_SITE 440 440 BY SIMILARITY.
ACT_SITE 561 861 BY SIMILARITY.
SEQUENCE 764 AA; 85325 MW; 6B45482E4A26BACF CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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              EMBL; L11647; AAA67437.1;
                                                                                                                                                                                                                                      Best_Local Similarity 24.2
Matches 133; Conservative
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GLGB OR SLL0158.
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P52981;
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Best Local S
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GLGB_SYNY3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DD----ASEIPDDPASRYQPEGVHGPSQIIQ-ESKEFNNETFLK------KEDLIIYEI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FEGVIRKLDYLKDLGITAIEIM 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGN- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 LAFFDGTHLYEHGDPRKGEHK-EWGTLIFNYG---RNEVRNFLVANALFWFDKYHIDGMR 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMYSWPIYVGGLGFNLKW-----DYFSMDPW 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRQFHQNSITFSMMYNHSE-----NYMLAL-SHDEVVH-GKSNMLGKMPGDEWQKYA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 VDGVKGVYFAVWAPNARNVSILGDFNNWDGRLHQMRKRNNMVWELFIPELGVGTSYKYEI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----YMVKLGPYFSQKYKTPWG-LTFNFDDAESDEVRKFILENVEYWIKEYNVDGFR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDAVASMLYLDYCREEGEWVANEYGGRENLEAADFLRQVNSVVYSYFPGILSIAEESTSW 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSNFRRKT------HGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 IDG-NEVIFTLWAPYQKSVKL----KVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL 61
                                                 Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Sequence analysis of the genome of the unicellular cyanobacterium Sequence analysis of the genome in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
SEQUENCE FROM N.A.
MEDLINE-96127529; PubMed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                       LDAVHAII------NTIVIAESDLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 2.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
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BY SIMILARITY.

A435AFCA7703FA8A CRC64;
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Pred. No. 1.9e-14;
; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
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23.1%; Pred
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770 AA;
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ACT_SITE 433 4
ACT_SITE 486 4
ACT_SITE 554 SEQUENCE 770 AA;
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Best Local Sim:
Matches 119;
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402 AALYLLS----PYIPMIFMGEEYGEENPFYFFSD 431

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326 HPFDGSWGYQVTGYYAATSRYGSPEDFMYFVDRCHQNGIGVILDWVPGHFPKDGHGLA-- 383
                                                                                                                                                                                                                                                                                                                                         349 KYSNFRRKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9829597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Bociphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
1-OCT-2096 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update).
Probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen
                                                  QXYKTPWG-LTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRL
                                                                                                                                               253 DAVHAI--IDTSPK-----IAESDLN
                                                                                                                                                                                                                                            289 DPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDG
                                                                                                                                                                                                                                                                          497 WPMVSWPTYVGGLGFNLKW-----DYFSMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         409 -----PYIPMIFMGEEYGE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 YMFTHPGKKTLFMGMEFGQ 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001)
                                          205 GPYFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 VNFAVWAPSARNVSILGDFNSWDGRKHQMARRSNGIWELFIPELTVGAAYKYEIKNYDGH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EIPDPASRYQPEGVHGPSQIIQESKEF--NNETFLK------KEDLIIYEIHVGTF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TPEGTF----EGVIRKLDYLKDLGITAIEIMPIAQ 144
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                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FDB-1995 (Rel. 31, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 VIFTLWAPYQKSVKL----KVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANBOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS APPROXIMATELY 35 DEGREES CELSIUS.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCC7942 branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 773;
                                                                                                                                                                                                                                                                                                                                       Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycogen biosynthesis; Transferase; Glycosyltransferase.
INIT_MET 0 0
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"Nucleotide sequence of the Synechococcus sp. PCC7942 kenzyme gene (919B): expression in Bacillus subtilis.";
Gene 89:77-84(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
SIMILARITY.
SIMILARITY.
52BAA17CA337BF57 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS. SUBUNIT: MONOMER.
| : | | : | | : | | NVRALETYMFTHPGKKTMFMSMEFGQWSEWNVWGD 611
                                                                                                                                          773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JQ0550; JQ0550.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; I.
Pfam; PF02922; isoamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90323609; PubMed=2142668;
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560
773 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1140;
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                                                                                                                                          GLGB_SYNP7
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ACT_SITE
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its S.L., STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam. A., Ermolaeva M.D., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., "Whole genome comparison of Mycobacterium tuberculosis clinical and -!- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS. -!- SUBUNIT: MONOMER (BY SIMILARITY). -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO of CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages to the EMBL/GenBank/DDBJ databases

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Best Loca
Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                  TFTPEGTFEGVIRKL-DYLKDLGITA1E1MPIAQFPGKRDWGYDGVYLYAVQNSYGGPEG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                      -VRDRYKYVLDDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DISPKHILEEIADVVHKY--NRIVIAESDLNDPRVVNPKEKCGYNIDAQWVD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNVHGGRENLEAVQFLQEMNATAHKVAPGIVTIAEESTPWSGVTRPTNIGGLGFSMKWNM 489
                                                                                                                                                                                                                                                                                                          12 VIFILWAPYQKSVKL--------KVL-EKGLYEMERDE---KGYFTITLNNVK- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                               147 VSFAVWAPNAKGVSLIGEFNGWNGHEAPMRVLGPSGVWELFWPDFPCDGLYKFRVHGADG
                                                                                                                                                                                                                                                                                                                                                                     SWRPGLSYRQLARELIDYIVDQGFTHVELLPVAEHPFAGSWGYQVTSYYAPTSRFGTPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRKLVDEAHKKGLGVILDVV-------YNHVGPEGNYMVKLGPYFSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 FRALVDALHQAGIGVIVDWVPAHFPKDAWALGRFDGTPLYEHSDPKRGEQLDWGTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VFDFG---RPEVRNFLVANALYWLQEFHIDGLRVDAVASMLYLDYSRPEGGWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLS----PYIPMIFMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 DFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKD-----VFVYDGKYSNFRKTHGEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWMHDT------LDYVSRDPVYRSYHHHEMTFSMLYAFSENY------
                                                                                                                                                                                                                                                             Score 326; DB 1; Length 731;
Pred. No. 5.4e-14;
; Mismatches 186; Indels 134;
                                                                                                                                              Glycogen biosynthesis; Transferase; Glycosyltransferase; Complete proteome.

ACT_SITE 461 464 BY SIMILARITY.

ACT_SITE 532 532 BY SIMILARITY.

CONFLICT 234 223 P -> A (IN REF. 2).

CONFLICT 233 223 P -> Q (IN REF. 2).
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BY SIMILARITY.

BY SIMILARITY.

P -> A (IN REF. 2).

EE2BFEF765352617 CRC64;
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InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                   10.9%; Scc_
22.8%; Pred
76;
                                                                                                                         Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                 AE007010; AAK45632.1; -.
                                                                                                                                                                                                                              M.
                                                       EMBL; Z73902; CAA98090.1;
                                                                                                                                                                                                                             81729
                                                                                                                                                                                                                                                                                   Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                        Tuberculist; Rv1326c;
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                            731 AA;
                                                                 EMBL; AE007010
TIGR; MT1368;
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P30539;
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                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                                                                                                                                                      Rumbak E., Rawlings D.E., Lindsey G.G., Woods D.R.;
"Characterization of the Butyrivibrio fibrisolvens glgB gene, which encodes a glycogen-branching enzyme with starch-clearing activity.";
J. Bacteriol. 173:6732-6741(1991).
-!- FUNCTION: TRANSFERS CHAINS OF 5 TO 10 (OPTIMUM, 7) GLUCOSE UNITS, USING AMYLOSE AND AMYLOPECTIN AS SUBSTRATES, TO PRODUCE A HIGHLY BRANCHED POLYMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I--PDPASRY---QPEGVHGPSQII----QESKEFNNETFLKKED-----LIIYEIHVGT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FT--PEGTFEGVI------RKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDAQWVDDFHHSIHAYLTGE---RQG--YYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycogen.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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Butyrivibrio fibrisolvens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Butyrivibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 321; DB 1; Length 639; 25.1%; Pred. No. 9.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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ACT_SITE 313 313 BY SIMILARITY.

ACT_SITE 366 BY SIMILARITY.

ACT_SITE 366 BY SIMILARITY.

SEQUENCE 639 AA; 73875 WW, DC93B72A5F28C2AF CRC64:
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                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                             MEDLINE-92041554; PubMed=1938880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M64980; AAA23007.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                NCBI_TaxID=831;
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                                MEDIATRE-95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Ferlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.T., Glodek A., Kellay J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Mismatches 173; Indels 186; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THIS PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/
CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS
  HGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.\,";
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BY SIMILARITY.
E2B71F610E8B1CAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Glycogen operon protein glgX (EC 3.2.1.).
                                                                                                                                                                                                                                                                                                              659 AA.
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InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; I.
Pfam; PF02922; isoamylase; I.
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57 YKYVLDDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKK--EDLIIYEIHVGTFT 114
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Search completed: July 15, 2002, 12:24:32 Job time: 384 sec

066936 aquifex aeo 004196 arabidopsis 08404 culamydia t 005152 aulfolobus 05243 bacillus st 0928f5 chlamydia m 09pxc6 chlamydia m p73608 synechocyst

Q9f930 streptococc

Q9ky06 streptomyce P58813 streptomyce P5883 streptomyce P5886 sulfolobus Q98594 rhizobium 1 Q22637 zea mays (m Q9m055 arabidopsis Q9733 sulfolobus Q9733 sulfolobus Q97405 bacillus ha Q97705 bacillus ha Q97093 bacillus sp P70983 bacillus sp Q91872 bacillus sp Q91872 bacillus sp Q91872 bacillus sp Q91872 zea mays (m Q91742 zea mays (m

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OM protein

Run on:

Sequence:

Searched:

Database

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Signature, State M., Miura Y., Komeda T., Konishi Y., Shindo K., Kobayashi K., Iwamatsu A.;

The gene analysis of the new amylases from the hyper thermophilic archae Sulfolobus."

Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

EMBL, D64130; BAALIO10:1:

InterPro; IPR004193; isoamylase.

InterPro; IPR004193; isoamylase.

Pfam; PF02922; isoamylase.N:

SEQUENCE 559 AA; 64790 MW; 79FBE23A7CD38B4E CRC64;
                                                                                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus
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                                                                    Q59832
P95868
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01-NAY-1997 (TrEMBLrel. 03
01-DEC-2001 (TrEMBLrel. 15
ALPHA-AMYLASE.
Sulfolobus solfataricus
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NCBI_TaxID=2287;
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             RESULT
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July 15, 2002, 12:17:38 ; Search time 55:94 Seconds (without alignments) 1728.712 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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09UWN9 P95867 053841 097344 097314 091821 091821 097345 097345 097345 093035 093039 093039

42.6 34.7 30.4 229.6 229.7 117.6 113.3 113.3 112.8 112.3

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Waltooligosyl trehalose trehalohydrolase from Sulfolobus shibatae.";
Submitted (NOV-1999) to the ENBL/GenBank/DDBJ databases.
EMBL, AF201335, AAF17553.1, F. InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase.
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Archaea; Crenarchaeota; Sulfolobales; Sulfolobus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALTOCLIGOSYL TREHALOSE TREHALOHYDROLASE.
TREZ
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Pfam; PF02922; isoamylase_N; 1.
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STRAIN-ATCC 35092 / DSM 1617 / P2;

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE=2133296; PubMed=11427726;

A Mayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Thi-Ngoc H.P., Reden P., Schenk M.E., Theriault C., Tolstrup N.,

A darrett R.A., Ragan M.A., Sensen C.W., Van dea Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2."

The Complete genome of the crenarchaeon Sulfolobus solfataricus P2."

EMBL: X08256, CAM69503.1;

EMBL: AE006815; AAK42272.1;

EMBL: AE006815; AAK42272.1;

InterPro; IPR000461; Alpha_amylase.

InterPro; IPR004191; isoamylase.
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(MALTO-OLIGOSYLTREHALOSE TREHALOHYDROLASE)
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PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1
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"Cloning and sequencing of a cluster of genes encoding novel enzymes of trehalose biosynthesis from thermophilic archaebacterium Sulfolobus acidocaldarius.";
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                                                 FEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEA
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL; D64131; BAA11011.1; --
EMBL; D83245; BAA11863.1; --
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR001493; isoamylase.N.
InterPro; IPR003625; sub_transporter.
Pfam; PF00128; alpha-amylase.N.
Pfam; PF00128; isoamylase.N.
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Pubmed-11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijina K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
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PUTATIVE ALPHA-AMYLASE.
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Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL589708; CAC33923.1; -
InterPro; IPR000461; Alpha_amylase.
Pfam: PF00128; alpha_amylase.
SEQUENCE 581 AA; 63952 MW; 8816DFF3BC1A3408 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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                                                                                          Length 359;
"Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNA Res. 8:123-140(2001).
BMBL; AP000984; BAB65939-1; --
Hypotherical protein; Complete proteome.
SEQUENCE 359 AA; 41600 MW; 4D9F429099E81665 CRC64;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                       ; Score 1269; DB 17; Length
; Pred. No. 1.1e-72;
51; Mismatches 71; Indels
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MEDLINE=97000351; PubMed=8843436;
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64.98;
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                                                                                                                            14 FTLWAPYQKSVKLKVLEKGLYEMERDEK--GYFTITLNNVKVRD--RYKYVLDDASEIPD 69
                                                                                                                                                                                  3 FEVWAPQAGRVTLR-CDGATRALERDPERPGWW---CGEAPARDGSRYGFAVDDGPVLPD 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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              Length 581;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2010 (TrEMBLrel. 19, Last annotation update)
MALTOOLIGOSYLTREHALOSE TREHALOHYDROLASE, PUTATIVE.
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InterPro; IPR004193; isoamylase_N.
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EMBL; AE001905; AAF10042.1;
TIGR; DR0464; -
                                                                    Matches 213; Conservative
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                                         Similarity
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SEQUENCE FROM N.A.
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Similarity
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Best Local S:
Matches 203;
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                                                                                                                                                                                       - PTPDPYARFLPDGVHGEAEVV----DFG--TFDWTDADWHGIKLADCVFYEVHVGTFTP 139
                                                                                                                                                                                                                         EGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLV 175
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MEDLINE-20143137; PubMed-10984043;
MEDLINE-20143137; PubMed-10984043;
STOREN G.K., Pham X.-0.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Santh K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                FRLWTSTARTVAVRVNGTEHVMTSLGGGIYELELP-----VGPGARYLFVLDGV 86
                                                                                                                          FTLWAPYQKSVKLKV-----LEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDA 64
                                                                                                                                                                                                                                      200 DAAHRIGLGVFLDVVYNHFGPSGNYLSSYAPSYFTDRFSSAWGM--GLDYAE-PHMRRYV
                                                                                                                                                                                                                                                                        DEAHKKGLGVILDVVYNHVGPEGNYMVKLGP-YFSQKYKTPWGLTFNFDDAESDEVRKFI
                                                                                                                                                                                                                                                                                                                        LENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKY--NRIVIAESDLNDPRV
                                                                                                                                                                                                                                                                                                                                               257 TGNARMWLRDYHFDGLRLDATPYMTDDSETHILTELAQEIHELGGTHLLLAEDHRNLPDL
                                                                                                                                                                                                                                                                                                                                                                                                                     352 NFRRKTH--GEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKL--VDRESYKIAAALYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 SPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKE-----NGQDT-DPQDES
                                                                          600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 TFNASKLSWKIDE----EIFSFYKILIKMRKELSIACDR-RVNVVNGEN 503
                                                                         DB 16; Length
                                                                                                 86; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
Hydrolase; Complete proteome.
SEQUENCE 600 Aa; 66909 MW; 594091EC093F8A44 CRC64;
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Last annotation update)
                                                                        30.4%; Score 905.5; DB 1
38.7%; Pred. No. 2.3e-49;
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                                                                                                 Conservative
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01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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                                                                                     Similarity
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                                                                                     Best_Local Sim:
Matches 205;
                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DDASEIPDPASRYQPEGVHGPSQIIQES - - - - KEFNNETFLKKEDLIIYEIHVGTFTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 DEAHKKGLGVILDVVYNHVGPEGNYMVK-LGPYFSQKYKTPWGLTFNFDDAESDEVRKFI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 LENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIA------DVVHKYNRIVIAE 284
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                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                  29.6%; Score 881.5; DB 16; Length
36.3%; Pred. No. 7.3e-48;
Live 95; Mismatches 174; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE 1,4-ALPHA-GLUCAN BRANCHING ENZYME PROFEIN (EC
                                                                                                                                                            651CD7A918833E00 CRC64;
EMBL, AE004643; AAG05552.1; -.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR00464; Alpha_amylase.
Pfam; PF00128; alpha_amylase.i.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
Hydrolas; PS00070; ALDEHYDE_DEHYDR_CYS; COMPLETE PSOFORCE.SB3 AA; 65557 WW; 651CD7A918833E00 C
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Transferase;
SEQUENCE 55
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Matches 132;
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Q44528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 RKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GVILDVVYNHVGPEGNYMVKLGP-YFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWI 242
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                              19 IDSDICRFREMAPDEREVDL-VLGGAVHKMQSLDGGWFEITL-AAKAGERYCFRLADGTE 76
                                                                                                                                                                                                                                                                                                                                  IDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASE 66
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 EGSRARVPPQGRVN-----FLQNHDQIGNRAFGERLASLLQEDSLRVLAAMHMLTPQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --RKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 FNASKLSWK----IDEEIFSFYKILIKMRK----------
                                                                                                                                       protein;
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                                                                                                                                                                                                                                                Length 601;
                                                                                                                                                                                                                                           Query Match 29.4%; Score 876.5; DB 16; Length Best Local Similarity 35.3%; Pred. No. 1.6e-47; Matches 207; Conservative 99; Mismatches 204; Indels
                                                                fixing endosymbiont Sinorhizoblum meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL, AL603646; CAC49676.1;
Transferase; Glycosyltransferase; Plasmid; Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 ELSIAC-DRRVNVVNGENWL-IIKGREYFSLYVFSKSSIEVKYSGTL 531
                                                                                                                                                                                024DA322A7B72C2E CRC64;
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Last sequence update)
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                                                                                                                                                                                601 AA; 66954 MW;
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01-DEC-2001 (TrEMBLTE1.
01-DEC-2001 (TrEMBLTE1.
01-DEC-2001 (TrEMBLTE1.
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ST0926.
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STRAIN-JCM 10545 / 7;
PubMed-11572479;
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Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 PASRYQPEGVHGPSQIIQESKEF-NNETFLKKEDLIIYEIHVGTFTPEGTFEGVIRKLDY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILD 188
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                                                                                                                                                                                                                                                                                                                       Length 217;
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NCBL_TaxID=1172;
                                                                                                                       "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; APO00984; BAB65938.1; --
Hypothetical protein; Complete proteome.
SEQUENCE 217 AA; 25181 MW; 4A1235EC5B491CEF CRC64;
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552 Aa; 63833 MW; 069886FAFD8FC411 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ALPHA-GLUCANOTRANSFERASE /HYDROLASE.
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Pred. No. 2.4e-37;
; Mismatches 36;
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Plant Mol. 18:165-170(1992).
EMBL; X59279; CAA41970.1;
InterPro: IPR000461; Alpha_amylase.
InterPro: IPR004193; isoamylase.N.
Pfant; PP00128; alpha-amylase.N.
Pfant; PF00222; isoamylase.N:
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66.0%; Pre
tive 28;
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EMBL; D87026; BAA19588.1;
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| HVGDFSGGEDDPYARGKYKHVIEKLDYLCELGINAIELLPVKEYPGDYSWGYNPRYFFAT 182
                                                                                                                                                                                 QNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNY-MVKLGPYFSQKYKTP---WG 217
                                                                                                                                                                                                                                               LTFNF----DDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHIL----EE 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 -FDLENLKDVI------DPKRQGF-----LGATNVVNYLTNHDHDHIMVEL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNRGKGERIIKLVDRESY---KIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKL 437
                                                                 HVGTFT-----PEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAV 161
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branching enzyme
                                                                                                                                                                                                                                                                                                                                                               303 TAGAKPFYN---VAEHIPETTSITNLDGPMDGC-----WHDSFYHTIKAHICGDT---
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01-NOV-1996 (TTEMBLrel. 01, Created)
01-NOV-1996 (TTEMBLrel. 01, Last sequence update)
01-BC-2001 (TTEMBLRel. 19, Last annotation update)
1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
GLYCOGEN BRANCHING ENZYME) (1,4-ALPHA-GLUCAN BRANCHING ENZYME)
(AMYLO-(1,4 1,0).15)-TRANSGLUCOSIDASE)
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MISCELLANEOUS: OPTIMAL ACTIVITY AT APPROXIMATELY 39 DEGREES
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
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MEDLINE=95031021; PubMed=7944355;
Takata H., Takaha T., Kuriki T., Okada S., Takagi I Properties and active center of the thermostable I from Bacillus stearothermophilus.";
Appl. Environ. Microbiol. 60:3096-3104(1994).
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Submitted (AUG-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EDLIIYEIHVGTF-TPEGTF----EGVIRKLDYLKDLGITAIEIMPIAQFPGKRD 150
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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               4 AYKIDGNEVI-----FILMAPYQKSVKL----KVLEKGLYEMER-DEKGYFTITLN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHV--GPEGNYMVKLGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YFSQKYKT--PWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAII----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DTSPKHILEEIADVVHKY--NRIVIAESDLNDPRVVNPKEKCGYNIDAQWVDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDRLYENPYAVEFLRKLNEAVFAYDPNALMIAEDSTDWPKVTAPTYEGGLGFNYKW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 VYIQN------PMIFMGERIIKLVDRESYKIAAALYLLSPYI-----PMIFMGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WKFEDELDWVLF
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Ucki T., Inouye S.;
"Identification of a new His-Asp phosphorelay signal transduction
                                                                                                                                                                                                                                                                                             13.4%; Score 3>>, 25.2%; Pred. No. 3e-17; tive 96; Mismatches 189; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FSFYKILIKMRKELSIACDRRVNVV-----NGENWLIIKGREYFSLYVF 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myxobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 DFELHRKMNDYMKEL-IACYKRYKPFYELDHDPQGFEWIDVHNAEQ-SIFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus
                                                                                                      Glycogen biosynthesis; Transferase, Glycosyltransferase.
ACT_SITE 308 308 BY SIMILARITY.
ACT_SITE 351 351 BY SIMILARITY.
ACT_SITE 419 419 BY SIMILARITY.
SEQUENCE 652 AA; 76793 MW, 4591BB414A0E3FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BRANCHING ENZYME GLGB (FRAGMENT).
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InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=34;
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43 YFTITLNNVKVRDRYKYVLD---DASEIPDPASR-----YQPEGVHGPSQIIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           saccharolyticus.
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01-NOV-1996 (
01-DEC-2001 (
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                                                                                                                                                                                            62 DDASEIPDPASRYQPEGVHGPSQIIQESKEF.-NNETFLKK--EDLIIYEIHVGTF--TP 115
                                                                                                                                                                                                            ---EGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFR 172
                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                           KLVDEAHKKGLGVILDVVYNHVGP-----EGNYMVKLGPYFSQKYK--TPWGLTFNF 222
                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                            DDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAI----IDTSPKHILEEIADVVHKY 277
                                                                                                                                                                                                                                                                                                                                                                                                                300 NREINATOPWKISIAEDFGGGDFITNDATSDTSGGAGFDSQWGGDFVHAIRAAVIAS--- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                           383
                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NDSGR---DMNSVRNAITQRYSGRHT------ARVIYSESHDEVAN- 393
                                                                                                                           Gaps
                                                                                                                                                                        67
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                                                                                                                                              14 FTLWAPYQKSVKLKVLEKGLY-----EMERDEKGYFTITLNNVKVRDRYKYVL---- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 DGNEVIFTLWAP------KQK-----SVKLKVLEKGLYEMERDE------KG 42
                                                                                                                                                                                                                                                         326 YYIDFGNLDDIVKSYKDVFV--YDGKYSNFRRKTHGEPVGELDGCNFVVYIQNHDQVGNR
                                                                                                                                                                     FRVWAP----MASRVFVSGDFNGWGTWIELGNEFNGNFSGDVAGAVKGQKYKFITRNQWG
                                                                                                                                                                                                                                                                                                                                                                   PDYGRPEVRAYIRDSMMNLTHSFRGDGLRWDATKYMRTQNGSDTT---AIPDAWRVFRSI
                                                                                                                                                                                                                                                                                                                                                                                            NR-----IVIAESDLNDPRVVN---PKEKCGYNIDAQWVDDFHHSIHAYLTGERQG
     of
                                                                                                                        98;
system which regulates expression of a heat shock gene, lonD, Myxococcus xanthus.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF285783; AAK83002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1142;
                                                                                                 Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKGERIIKLV-----DRESYKIAAALYLLSPYIPMIFMGEEYGE 422
                                                                                                                       75; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "alkaline pullulanase from the alkaliphilic bacterium.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049812; BAB47586.1; -.
SEQUENCE 1142 AA; 128759 WW; 318FC01362961E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                            440 AA; 48964 MW; 8D492EA5A4A92017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 395.5; DB 2;
larity 22.9%; Pred. No. 1.1e-16;
Conservative 100; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=72413;
                                                                                               13.3%; Score 397; DB 2; 28.0%; Pred. No. 2.3e-17;
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                                                                                                            Best Local Similarity 28.09
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sp. KSM-1876.
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PUL1876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hatada Y., Ito S.;
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01-DEC-2001
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                                                            SEQUENCE
                                                                                                 Query Match
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Matches
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ESKEFNNETFLKKEDLIIYEIHVGTFTPE------GTFEGVIRKLDYLKDLGITA 136
                                                                                                                                           IEIMPIAQF----GPGKRD-----G 170
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                                                                                                                                                                                                                                                                                                                793
                                                                                                                                                                        IQLLPVMSYFFANEFKNDERMLDFSSTNTNYNWGYDPQSYFALTGMYSEDPTDPELRIKE 602
                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                      315 IHA-----YLTGERQGYYTDFGNLD---DIVKSYKDVFVYDGKYSNFRRKTHGEPV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GELDGCNFVVYIQNHDQVGNRGKGERIIKLVDR-----ESYKIAAALYLLSPYIP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EEN--PF---YFFSDFSDSKLIQGVREGRKK 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGQDTDPQDEST-----FNASKLSWK -- IDEEIFSFYKILIKMRKELSIAC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      saccharolyticus).
                              YY-----YHYEIDHDGDKKIALDPYAKSLSAWNSDEQGPYAKAAIVDPSSIGP
                                                                                           FRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAES ---
                                                                                                                                                                                                                                                                                                                                                                   276 KY----NRIVIAE-----SDLNDPRVVNPKEKCGYNIDAQWV-----DDFHHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 FLHAGQEYGRTKQFRAETSEPPYKSTYMTDENGEPFRYPYFIHDSYDSTDIINRFDWERA
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L39876; AAB06264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albertson G.D., McHale R., Gibbs M.D., Bergquist P.L., "Cloning and expression of a type II pullulanase from a thermophilic anaerobic bacterium, Caldicellulosiruptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-DEXTRIN 6-GLUCANOHYDROLASE (EC 3.2.1.41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caldocellum saccharolyticum (Caldicellulosiruptor Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacter group; Caldicellulosiruptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 MIFMGEEYG------
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31;
                                                                                                                                                                                    220 FRLWAPTAYKVKIQIFDEHENFKFGKEMSRAENGTWDVYLPGDLKNHFYLYEIWHYNYED 279
                                                                                                                                                                                                                       64 ----ASEIPDPASRYQPEGVHGPSQIIQES----KEFNNETFL----KKEDLIIYEIHV 110
                                                                                                                                                                                                                                        280 DEGYIVYHVPDPYSKASSSN-SGKSYIFDPADGLIDGWQADSFVDNIEKQDDAIIYEMHV 338
                                                                                                                                                                                                                                                                              111 GTFT------ 145
                                                                                                                                                                                                                                                                                              194 ------VGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVFVYDGKYSNFRRKTHGEPVGELDGCNFVVYIQNHDQVGNRGK-----GERIIKLVDR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.8%; Score 381.5; DB 2; Length 825; Best Local Similarity 25.7%; Pred. No. 5.2e-16; Matches 149; Conservative 86; Mismatches 170; Indels 175; Gaps
                                                                                                                                                                                                                                                                                                                                   146 --PGKR-DWGYDGV----YLYAVQNSYGGPEGFRKL---VDEAHKKGLGVILDVVYNH 193
                                                                                                                                                                                                                                                                                                                                                                                                         396 ESYKIAAALYLLSPYIPMIFMGEEY----GEENPFYFFSDFSDSKLIQGVREGRKKENG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                               240 YWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYN------RIVIAESDLNDPR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 VVNPKEKC--GYNIDAQWVDDFHHSIHAYLTGERQGYYTDF--GNLDDI-----VKSYK 341
                                                                                                                                                                   FTLWAPYQKSVKLKVLE-----KGLYEMERDEKGYFTITL-----NNVKVRDRYKYVLDD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN------
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
Hydrolase; Glycosidase.
SEQUENCE 825 AA; 95732 MW; 92C2082E9B35F5AD CRC64;
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GenCore version 4.5
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                                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2954
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Perfect score:
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111: /SIDSI/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
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127: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:* 110: 111: 112: 113: 114: 115: 116: 116: 119: 119: 120:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Trehalose-releasin	Sulfolobus acidoca	Sulfolobus solfata	C qlutamicum prote	Corynebacterium ql	Trehalose releasin	Trehalose releasin	Trehalose releasin	Trehalose releasin	Trehalose-releasin	Trehalose-releasin
SUMMARIES	AAR92755	AAR90620	AAR90619	AAG92072	AAB80206	AAR80289	AAR77470	AAR77471	AAR80290	AAY85157	AAY85165
DB	17	17	17	22	22	16	16	16	16	21	21
% Query Match Length DB	556	556	559	595	610	589	296	598	597	575	575
% Query Match	100.0	100.0	59.2	35.3	35.3	32.8	32.8	32.5	32.4	31.7	31.7
Score	2954	2954	1748.5	1042.5	1042.5	696	696	959	928	936	936
Result No.	г	2	n	4	S	9	7	œ	σ	10	11

	Starch-branching-e	Heat-resistant pul	-	υ			The	Thermotoga		Gro			Propionibacterium	s.	C. pneumoniae	Sed	A polypepti				Bacillus	Pullulana	Wheat isoamy		Full length		Bacillus	Original	Protein in	Bacillus acidopul	Bacillus	N. denitr	כתמ
AAR80037	AAR96109	AAR23787	AAR11271	AAG91100	AAB79423	AAP94635	AAW34567	AAW49871	AAY00869	AAY91279	AAU60913	AAW36602	AAU60903	AAY00870	AAY34991	AAP91904	AAB19285	AAY17523	AAB69074	AAY27357	AAE05691	AAY78513	AAY50819	AAW73552	AAW73553	AAW09257	AAW09255	AAY00872	AAY37184	AAE05723		AAW90977	AAE05689
16	17	13	12	22	22	10	18	19	20	21	22	18	22	20	20	10	21	20	22	20	22	21	21	20	20	17	17	20	20	22	22	21	22
652	652	658	639	731	731	648	772	772	793	1250	670	909	718	166	999	562	621	818	630	931	829	862	764	798	1938	893	1938	931	618	921	921	762	921
12.2				11.4				10.9			10.6	10.5	10.4	10.4				•		٠		6.6				٠	•		9.4	9.4		9.3	9.3
360	9	S	342.5	3	336	•	323	321	32	313.5	312	310.5	306	306	303.5	301	298.5	296.5	296	293.5	292	292	285	284	284	282	282	280.5	<u>.</u>	277	277	276	276
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

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Sulfolobus acidocaldarius strain ATCC 33909. Thermostable enzyme; trehalose; sweetener. Trehalose-releasing thermostable enzyme. (HAYB) HAYASHIBARA SEIBUTSU KAGAKU. AA. AAR92755 standard; Protein; 556 95JP-0189760. 94JP-0190180. 95JP-0109128. 95AU-0027131. (first entry) 04-JUL-1995; 21-JUL-1994; 11-APR-1995; 21-JUL-1995; 03-AUG-1996 AU9527131-A. 01-FEB-1996. AAR92755; AAR92755

Sugimoto Kubota M, Mitsuzumi H, WPI; 1996-106284/12. N-PSDB; AAT16899.

Recombinant thermostable enzyme from Sulfolobus acidocaldarius, releases trehalose from non-reducing saccharide at temps, exceeding 55 degrees Centigrade

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                                                                                                                                                                                                                                                                                                                                                                                                                         GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYE 420
                        A thermostable enzyme (AAR92755) of Sulfolobus acidocaldarius ATCC 33909 releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of polymerisation of at least 3. It has a mol.wt. of 54.64 kps (SDS-PAGE), a pl of 5.6-6.6 and is substantially not inactivated when incubated in acolution (pH 7.0) at 85 deg for 60 min. Recombinant enzyme is obtd. by expression of an isolated DNA fragment (AAT16899) in host cells, pref. Escherichia coli, using e.g. vector pBluescript II SK(+). The trehelose is useful as a sweetener.
                                                                                                                                                                         Gaps
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                                                                                                                                                                                                     1 MFSFGGNIEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus acidocaldarius amylase for alpha, alpha-trehalose prodn.
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                                                                                                                                                                        ó;
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                                                                                                                                                                        Indels
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                                                                                                                                                      Score 2954; DB 17;
Pred. No. 7.5e-267;
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         53-54; 74pp; English.
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100.0%;
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Matches 556; Conservative
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The amylase is derived from Sulfolobus acidocaldarius. The amylase acts on a saccharide having at least three sugar units, which are prefigurose units at the reducing end (the linkage between the first and second glucose units is alpha-1, alpha-1, while the linkage between the second and third glucose units is alpha-1, while the linkage between the linkages within the sugar chain, yielding alpha, alpha-trehalose and also mono- and disaccharide hydrolysis products. The amylase has a mol. wt. of 61 to 64 kDa. It is characterised by working at pH 4.5-5.5 and at 60-85 deg.C. It has an isoelectric point of 4.3-5.4 and retains at least 100 percent activity after 6 hrs. at 80 deg.C. It is completely inhibited by 5 mM copper sulphate. Use of a transferase and the amylase in succession on suitable substrates such a malto-oligosaccharides, is useful for the production of alpha, alpha-trehalose.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus spp. derived transferase and amylase - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha, alpha-trehalose from malto-oligosaccharide(s)
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94JP-0290394.
94JP-0286917.
94JP-0311185.
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acidocaldarius
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Best Local Simi
Matches 556;
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21-NOV-1994
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Sulfolobus
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                                                                                                                                          122 VIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKR
                                                                                                                                                                                                           182 GIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYW
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                SFGGNIEKNKGIFKLWAPYVNSVKLK-LSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII
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Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 595
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2000JP-0280988
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organic acid synthesis.
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03-AUG-2000;
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amylase is derived from Sulfolobus solfataricus. The amylase acts on a saccharide having at least three sugar units, which are prefigurose units at the reducing end (the linkage between the first and second glucose units is alpha-1, alpha-1, while the linkage between the second and third glucose units is alpha-1, 4), to hydrolyse alpha-1, 4 linkages within the sugar chain, yielding alpha, alpha-trehalose and also mono- and disaccharide hydrolysis products. The amylase has a mol. wt. of 61 to 64 kDa. It is characterised by working at pH 4.5-5.5 and at 60-85 deg.C. It has an isoelectric point of 4.3-5.4 and retains at least 100 percent activity after 6 hrs. at 80 deg.C. It is completely inhibited by 5 mw copper sulphate. Use of a transferase and the amylase in succession on suitable substrates such a malto-oligosaccharides, is useful for the production of alpha, alpha-trehalose.
                                                                                                             361 gdlpprkfvvfignhdqvgnrgngerlsiltdkttylmaatlyilspyiplifmgeeyye 420
                                                                                                                                                                                                                                                                                                                                                                                                        transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose;
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                              NIRKRYNNCKRVKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNLLIGIGFPKKLKK
                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus amylase for alpha, alpha-trehalose prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1748.5; DB 17; Length 559;
; Pred. No. 2.9e-154;
87; Mismatches 136; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus spp. derived transferase and amylase - fo alpha, alpha-trehalose from malto-oligosaccharide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                           malto-oligosaccharide; hydrolysis
                                                                                                                                                                                                                                                                          AAR90619 standard; Protein; 559
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Best Local Similarity 58.9%;
Matches 329; Conservative 87
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94JP-0194223.
94JP-0290394.
94JP-0286917.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                             DELIKVNRGVGVYQLE 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus solfataricus
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21-NOV-1994;
21-NOV-1994;
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AAB80206 standard; Protein; 610 AA
                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacteria are useful for producing amino acids, nucleic acids, vitemins, saaccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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40.8%; Pred. No. 2.7e-88;
1ve 93; Mismatches 199; Indels 35; Gaps
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                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO: 5826; 246pp + Sequence Listing; English.
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N-PSDB; AAH67291
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Best Local S
Matches 225,
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fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purhe base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                    protein;
                                                   Corynebacterium glutamicum MP protein sequence SEQ ID NO:1146
                                                                   Corynebacterium glutamicum; metabolic pathway protein; MP
                                                                                                                                                                                                                                                    99DE-1031424
99DE-1031428
99DE-1031434
99DE-1031443
99DE-1031443
99DE-1031453
99DE-1031465
99DE-1031510
99DE-1031510
99DE-1031573
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99DE-1031418.
99DE-1031419.
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99DE-1040764.
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                                                                                                                      Corynebacterium glutamicum
                                 (first entry)
                                                                                                                                      WO200100843-A2
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08-70L-1999;
08-70L-1999;
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03-SEP-1999;
03-SEP-1999;
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27-AUG-1999;
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176 NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL 235
524 ITGNLLIGIGFP 535
                          579 lggeliysftsp
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                                                                                                                                                                                                                                                                                                             F71753 to AAF72330 encode the Corynebacterium glutamicum metabolic thway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum nucleic acids are useful for the production of fine chemicals
                                                                                                                                                                                                                          pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
                                                                                                                                                                                                                                                                                                                                                      in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, uncleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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fsvwaplphdvhlilngetlpmhktegswwraeiap-kagdrygfslfdgsswsktlpdp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ASRYQPLGVHDKSQLIRTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVIEKLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Gaps
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                                                                                                                                         Haberhauer
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40.8%; Pred. No. 2.8e-88;
ive 93; Mismatches 199; Indels
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                                                                                                                                        Zelder
                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                  Claim 20; Page 1722-1725; 1737pp; English.
                                                                                                                                        Schroeder H,
                                     99DE-1042095.
99DE-1042124.
99DE-1042129.
2000US-0187970.
             99DE-1042087.
99DE-1042088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.3%
Best Local Similarity 40.8%
Matches 225; Conservative
                                                                                                                                        Kroeger B,
                                                                                                                                                                 2001-137957/14
                                                                                                                                                                                                            Nucleic acids from
                                                                                                                                                                                                                                                                                                                                                                                                                             610 AA;
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N-PSDB; AAF72325
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                                                                  03-SEP-1999;
09-MAR-2000;
                                                                                                            (BADI ) BASF
                                     03-SEP-1999;
03-SEP-1999;
                                                                                                                                        Pompejus M,
                          03-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a trehalose releasing enzyme – which releases trehalose from a non-reducing saccharide having a trehalose structure as an
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                                                                                                                                                                                                                                                   trehalose; alpha-qlucosyltrehalose; alpha-maltosyltrehalose;
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                                                                                                                                                                                                                                                                             alpĥa-maltotriosyltreĥalose; alpĥa-maltotetrasyltreĥalose;
maltopentaosyltreĥalose; sweetener; taste-improving agent;
stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 21-22; 45pp; English.
standard; Protein; 589
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ENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGK-----FVIAESDLND 289
                                    PKIV--KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK 347
                                                                                                                                      SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA 458
                                                                                                 348 YSRYRGRIHGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLXIL 405
                                                                                                                                                                         FLKSKLSWK-----IDEEVLDYYKOLINIRKRYNNCKRVKEVRREGNCITLIMEKIGIIA 513
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taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
                                                                                                                                                                          Gaps
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                                                                                                                             32.8%; Score 969; DB 16; 39.5%; Pred. No. 2e-81;
                                                                                                                                                                        74; Mismatches 195;
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                                                                                                                                                   Similarity
                                                             596 AA;
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This enzyme can be used for the preparation of trehalose with high yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose, alpha-maltotetrasyltrehalose and maltopentacosyltrehalose. The trehalose can be used as a sweetener, taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
                                                                                            trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
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maltopentaosyltrehalose; sweetener; taste-improving agent;
stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
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non-reducing saccharide having a trehalose structure as
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94JP-0059834
                                                                  Trehalose releasing enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV-----IAESDLNDPKIV--KD 295
                                                                                                                                                                                                                                       This enzyme can be used for the preparation of trehalose with high yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltotsyltrehalose, alpha-maltottriosyltrehalose. The translote used as a sweetener, maltopentaosyltrehalose. The trehalose can be used as a sweetener, taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDPASRYQPLGVHDKSQLI-RTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 mgeeygastpwqfftshpepelgkataegrikefermgwdpavyddpgdpetfrrskldw 497
                                                                                                                                                           oding a trehalose releasing enzyme – which releases trehalose non-reducing saccharide having a trehalose structure as an
                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKLWAPYVNSVKLKLSKKLIPMEK -----NDEGFFEVEIDDIEENLTYSYIIE-DKREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ydvwapnaesvtllaggeryamgrraetgpedagwwtaagaptdgnvdygylldgdetpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK
                                                                                                                                                                                                                                                                                                                                                                                          Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                      32.5%; Score 959; DB 16;
llarity 40.2%; Pred. No. 1.7e-80;
Conservative 81; Mismatches 186;
                                                                                           χ.
                                                                                           Sugimoto T, Tsusaki
                                                                 (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                              Claim 6; Page 27-29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIDEE-----VLDYYKQLINIRK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 aeaaegdharllelyrsltalrr
 95EP-0301474
                          94JP-0059840
                                      94JP-0059834
                                                                                          Kubota M,
                                                                                                                   WPI; 1995-312772/41.
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                  598 AA;
                                                                                                                                  N-PSDB; AAQ98672
                                                                                                                                                            encoding
07-MAR-1995;
                                      07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     Local Simines 202;
                        07-MAR-1994
                                                                                          Hattori K,
                                                                                                                                                                                       end unit
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                         from a
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Matches
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Tsusaki

Sugimoto T,

95EP-0301474

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 PDPASRYQPLGVHDKSQLI-RTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV-----IAESDLNDPKIV--KD 295
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                     Length 597;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                              186;
                                                                                                                                                                                                              ; Score 958; DB 16;
; Pred. No. 2.1e-80;
81; Mismatches 186;
                                                                                                                                                                                                                             32.4%;
40.2%;
                                                                                                                                                                                                                                                                                          Local Similarity 40.2
597 AA;
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AAR80290 standard; Protein; 597 AA.

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RESULT

AAR80290 ID AAR8

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This sequence represents a trehalose-releasing enzyme amino acid sequence from Arthrobacter sp. 534. This enzyme specifically hydrolyses a non-reducing saccharide having a trehalose structure as an end unit. The invention relates to this enzyme and also to a non-reducing saccharide forming enzyme that forms a non-reducing saccharide having a trehalose structure as an end unit by reducing partial starch hydrolysates. The two extracture as an end unit by reducing partial starch hydrolysates. The two moles of glucose bound at their reducing residues. The disaccharide is substantially free of reducibility and has moisture retaining abilities. The enzymes are used to produce non-reducing sugars they are particularly used for further enzymatic conversion of starch hydrolysate to trehalose. The non-reducing sugars produced by the enzymes are useful in foods, pharmaceuticals and cosmetics. Non-reducing sugars are compatible with anino acids and proteins, they do not cause browning, and have good moisture-retaining properties. The enzymes broduce the non-reducing sugars in high yield and function at a medium temperature range 1.e. between 40 degrees celsius and 60 degrees celsius, and in an acidic pH range, 1.e. a pH of less than 7. Production of non-reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-reducing saccharide-forming enzyme; trehalose; disaccharide; food; high yield; trehalose releasing enzyme; moisture retention; cosmetic;
HGAPV -- GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF 413
                                                                                                                       MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM -----IDPQSEEAFLKSKLSW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mesophilic enzyme from Arthrobacter, used to convert starch hydrolysate into non-reducing sugars, particularly trehalose, useful a sweetener in foods, pharmaceuticals and cosmetics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyake T;
                                                                                                                                                                                                                                                                                                                                                                                                                      Trehalose-releasing enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kubota M, Fukuda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Page 47-48; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                AAY85157 standard; protein; 575 AA
                                                                                                                                                                                                              497 aeaaegdharllelyrsltalrr 519
                                                                                                                                                                                          467 KIDEE-----VLDYYKQLİNIRK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0307220.
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98JP-0352252.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arthrobacter sp. S34.
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N-PSDB; AAA10503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         high yield; 
production.
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                                                                                                                                                                                                                                                                                                                                                   AAY85157;
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                                                                                                                     414
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                                                                                                                                                                                                                                                            QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKL 174
                                                                                                                                                                                                                             235 LENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIA----EKAHQLGK--FVIAESDLN 288
                                                                                                                                                                                                                                                                                                                     DPKIVKDDC--GYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDG 346
                                                                                                                                                                                                                                                                                                                                                                  347 KYSRYRGRTHGAPVG-DLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                                                                                                                                                                406 SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM------IDPQSEEA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                     ------KIEDLIIYELHVGTFS 114
                                                                                                                         15 FKLWAPYVNSVKLKL--SKKLIPMEKNDEGFFEVE--IDDIEENLTYSYIIEDKREIPDP 70
                                                                                                                                      sugars using the enzymes eliminates the need to convert a starch hydrolysate into sugar alcohols (non-reducing) by catalytic
                                                                                                    54;
                                                                              Length 575;
                                                                                                    Indels
                                                                            31.7%; Score 936; DB 21;
38.7%; Pred. No. 2.3e-78;
ive 82; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trehalose-releasing enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 FLKSKLSWKIDEE-----VLDYYKQLINIRK 484
                                                                                                                                                                     71 ASRYQPLGVHDKSQLIRTDYQILDLGKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY85165 standard; Protein; 575
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                                                                                         Best Local Similarity 38.7
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S34.
                                          575 AA;
                      hydrogenation.
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11-DEC-1998;
26-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arthrobacter
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                                            Sequence
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                                                                              Query Match
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412 gpftpmlfmgeewgartpwqfftshpepelgeatargriaefarmgwdpavvpdpgdpat 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 vpenleghlykyeivtpdgqvlfkadpyafyselrphtas--iaydlkgyqwndgswkrk 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 ----KVKIEDLIIYELHVGTF-SQEGNFKGVIEKLD----YLKDLGITGIELMPVAQFPG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 PYF----SDRYKIPWGLIFNFDDRGCDQVRKFILENVEYWFKIFKIDGLRLDAV---- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 drswgyggtgyyavtsrygtphdfmyfvdrchqagigvimdwvpghfckdahglymfdga 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable branching enzyme gene and recombinant plasmid contg. it — used to produced a thermostable branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gene coding for a thermostable branching enzyme has been isolated from chromosomal DNA of B.stearothermophilus strain TRBE14 and sequenced (see AAT04542). The enzyme (AAR80037) was found to have an activity of 80% or more at up to 65 deg.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 fgahvineggkvgtrfcvwapharevrlvgsfndwdgtdfrlek-----vndegvwtiv 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 FGGNIEKNKG----IFKLWAPYVNSVKL--------KLSKKLIPMEKNDEGFFEVE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 NRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 IDDIEENLTYSY-IIEDKREI---PDPASRYQPLGVHDKSQLIRTD---YQILDLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186; Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Met residue corresponds to TTG codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 652;
                                                                                                                                                                                                                                                                                                                                                                                   Thermostable; 1,4-alpha-glucan; branching enzyme; amylose;
                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus thermostable branching enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 360; DB 16;
Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.2%; Sco. 25.3%; Pred. No. 1., 25.3%; Pred. No. 1., 25.3%; T2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus (strain TRBE14).
                                          459 FLKSKLSWKIDEE-----VLDYYKQLINIRK 484
                                                                        Location/Qualifiers
                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 6-12; 14pp; Japanese.
                                                                                                                                                                                                    AAR80037 standard; Protein; 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0311004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93JP-0311004
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EZAK ) EZAKI GLICO CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT04542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          amylopectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP07213287-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1993;
                                                                                                                                                                                                                                                                                            11-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-1995
                                                                                                                                                                                                                                                AAR80037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                          RESULT 12
                                                                                      472
                                                                                                                                                                               AAR80037
qq
                                          Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abilities. The enzymes are used to produce non-reducing sugars, they are particularly used for further enzymatic conversion of starch hydrolysate to trehalose. The non-reducing sugars produced by the enaymes are useful in foods, pharmaceuticals and cosmetics. Non-reducing sugars are compatible with amino acids and proteins, they do not cause browning, and have good moisture-retaining properties. The enzymes produce the non-reducing sugars in high yield and function at a medium temperature range i.e. between 40 degrees celsius and 60 degrees celsius, and in an sugars using the enzymes eliminates the need to convert a starch hydrolysate into sugar alcohols (non-reducing) by catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                               from Arthrobacter sp. S34. This enzyme specifically hydrolyses a non-reducing saccharide having a trehalose structure as an end unit. The invention relates to this enzyme and also to a non-reducing saccharide forming enzyme that forms a non-reducing saccharide having a trehalose structure as an end unit by reducing partial starch hydrolysates. The two enzymes can be used to produce trehalose, a disaccharide consisting of two moles of glucose bound at their reducing residues. The disaccharide is substantially free of reducibility and has moisture retaining
                                                                                                                                                                                                                                                                                                               This sequence represents a trehalose-releasing enzyme amino acid sequence
                                                                                                                                                                        New mesophilic enzyme from Arthrobacter, used to convert starch hydrolysate into non-reducing sugars, particularly trehalose, useful as a sweetener in foods, pharmaceuticals and cosmetics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 ASRYQPLGVHDKSQLIRTDYQILDLGKV--------KIEDLIIYELHVGTFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 VNEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIA----EKAHQLGK--FVIAESDLN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPKIVKDDC--GYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 KYSRYRGRTHGAPVG-DLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 FKLWAPYVNSVKLKL--SKKLIPMEKNDEGFFEVE--IDDIEENLTYSYIIEDKREIPDP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :||| | | : : :|: ::: |: :| || || 5 fpwwapqaaqvtlvvgqgraelpltrdengwwalqqpwdggpdlvdygylvdgkgpfadp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                 ij
                                                                 Miyake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 936; DB 21;
38.7%; Pred. No. 2.3e-78;
tive 82; Mismatches 177;
                                                               Kubota M, Fukuda S,
                                                                                                                                                                                                                                                                Example 6-2; Page 56-58; 93pp; English.
                     (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                               Maruta K,
                                                                                                         2000-273225/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
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                                                                                                         WPI; 2000-273225,
N-PSDB; AAA10516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrogenation.
                                                               /amamoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                   256 ----HAIFDNS-PKHILQEIAEK--AHQLGKFVIAESDLNDPKIVKD-----DCGYKID 302
                                                                                  303 AQWVDDF-----HHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYR 352
                                                                                                                                   GRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNG---ERLSILTDKTTYLMAATLYILSPYI 409
                                                                                                                                                                                     410 PLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSW--- 466
                                                                                                                                                                                                   |:||| |: : : | | | 457 kllfmgnef-----aqfdewkfedeldwylf 482
                                                                                                           376 mgwmndmlkymetppyerrhvhnqvtfsllyays----enfilpfshdevvhgkks--- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New glucan with cyclic, branched core and outer branched region -useful in foods, drinks, adhesives, infusion compsns. etc., readily soluble in water forming solns. of low viscosity
                                                                                                                                                                                                                                                                                                                                                                                                                         Starch-branching-enzyme; thermostable; Q-enzyme; Escherichia coli; starch; amylopectin; glucan; cyclodextrin; food; food-additive; adhesive; biodegradable plastic.
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus strain TRBE14 (FERM P-13916).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Conserved amylase sequence used construct primer AAT27127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takaha T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Conserved amylase sequence"
414..423
/note= "Conserved amylase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Conserved amylase sequence construct primer AAT27126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura H,
Yanase M;
                                                                                                                                                                                                                                      --KIDEEVLDYYKQLINIRKRY 486
                                                                                                                                                                                                                                                   :: :: || |:|| ||| 483 dfelhrkmndymkeliacykry 504
                                                                                                                                                                                                                                                                                                                          AAR96109 standard; Protein; 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95JP-0195647.
94JP-0218554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95EP-0250222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EZAK ) EZAKI GLICO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309..317
                                                                                                                                                                                                                                                                                                                                                                                                  Starch-branching-enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Imanaka T,
Terada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-223407/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT27128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1995;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3P710674-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujii K, :
Takata H,
                                                                                                                                                                                                                                                                                                                                                  AAR96109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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This sequence represents a thermostable starch- branching-enzyme (Q-enzyme, EC-2.4.1.8) from Bacillus stearchermophilus TRBE14 (FERM P-13916). Conserved regions present in amylases are used to construct primers AAT27126-7, which are used in PCR to amplify a fragment of the gene, which is then used as a probe to isolate a full-length clone in Escherichia coli. The recombinant enzyme may be reacted with starch or amylopectin to produce a glucan with a degree of polymerisation of at least 50, with an inner branched cyclic region and an outer branched region. The product is freely soluble in water, forming a low-viscosity solution, is more resistence to degradation than native starch, does not react with proteins and amino acids, and is degraded to glucose in vivo, so is easily digestible. The glucan may be used in foods, beverages, food-additives, adhesives, in cyclodextrin production and as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 vpenleghlykyeivtpdggvlfkadpyafyselrphtas--iaydlkgygwndgswkrk 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 NRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLGLG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HAIFDNS-PKHILQEIAEK--AHQLGKFVIAESDLNDPKIVKD-----DCGYKID 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQWVDDF------HHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 PLIFMGEEYYETNPFFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSW--- 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :| : :| |
---aqfdewkfedeldwvlf 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 mgwmndmlkymetppyerrhvhngvtfsllyays----enfilpfshdevvhgkks--- 427
                                                                                                                                                                                                                                                                                                                                                             12.2%; Score 360; DB 17; Length 652;
25.3%; Pred. No. 1.7e-24;
ive 72; Mismatches 186; Indels 162; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGGNIEKNKG----IFKLWAPYVNSVKL------KLSKKLIPMEKNDEGFFEVE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KVKIEDLIIYELHVGTF-SQEGNFKGVIEKLD----YLKDLGITGIELMPVAQFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----hpgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDDIEENLTYSY-IIEDKREI---PDPASRYQPLGVHDKSQLIRTD---YQILDLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYF----SDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 GRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNG---ERLSILTDKTTYLMAATLYILSPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR23787 standard; Protein; 658 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: :: || |:|| |||
483 dfelhrkmndymkeliacykry 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 --KIDEEVLDYYKQLINIRKRY 486
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.3%
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                      652 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLD---YYKQLINIRKRYNNCKRVKEVRR 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLIIYELHVGTF--SQEGNF----KGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 GVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLGLGPYF---- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This branching enzyme is derived from B.stearothermophilus and is encoded by the glgB gene. It is stable at high temps. and can be produced in large amts. using recombinant techniques. It is a transferase allowing formation of alpha(1-6) branches in starch-like substances. It is useful for extending the shelf life of such materials and can be used in the prepn. of human and animal foods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Branching enzyme obtd. from Bacillus stearothermophilus - has good thermostability, for use in modifying starch-like substances
                                                             11.6%; Score 342.5; DB 12; Length 639; 24.9%; Pred. No. 7.2e-23; ive 89; Mismatches 197; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                      Branching enzyme; amylaceous substances; transferase;
482 gheseq----trkkrqklataivllsqgipflhsgqefyrtk--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venema G;
                                                                                                                                                                                                                                                                                                                                                                 B.stearothermophilus branching enzyme
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                                                                                                                                                                                                                                                639
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                                                                                                                                                                                                                                                AAR11271 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sacillus stearothermophilus
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Matches 135; Conser
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44 ffydgdlgvaytrektifkvwaptatevkvklidpktekaeyialerlekgvwtttvfgd 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 YRGRTHGAPVGD-----QVGN 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 RGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVR 440
                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid. The heat-resistant pullanase can be produced in large amts. using a sultable host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 EENLTYSYII----EDKREIPDPASRYQPLGVHDKSQLIRTDY-QILDLGKVKIE----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELMPVAQFPG------NRDWGYDGVFLYAVQNTY----GGPW----ELAKLVNEAHKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 silvfgegwdlptp-----lssegkatmqnaeklpri-gyfndyfrdsvkgst 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fqlpdrgfalgdsddrekvkvaisgsigkknglflhptqtinyveshdnhtfwdkmeian 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid prpI contg. the pullanase gene (Japan Patent Apppln. No. 174037/88) was cleaved by various restriction enzymes and inserted into plasmid pV118/119. Single-stranded DNA was prepd. using helper phage M13K07 and the base sequence determined by the dideoxy method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FSFGGNI----EKNKGIFKLWAPYVNSVKLKL----SKKLIPMEKNDEGFFEVEIDDI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DLIYELHVGTF-----SQEGNFKGVIEK------LDYLKDLGITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ellpfndfagvdernplqqynwgynplhynapegsyatdpndpyarirelkraihtlgsn
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330 rkwlidsvrfwveeyhvngfrfdlm-gildvetmkavreml-------dtldp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 356; DB 13; Length 658; 22.9%; Pred. No. 4.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 2-3; 8pp; Japanese
                                                                                                                                                                   90JP-0077230.
                                                                                                                                                                                                           90JP-0077230.
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                                                                                                                                                                                                                                              (EZAK ) EZAKI GLICO CO. (IATR ) IATRON LAB INC.
                                                                                                                                                                                                                                                                                                      WPI; 1992-157263/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             658 AA;
                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR23787
                   Enzyme; pTPI.
                                                                                        JP04099489-A
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Matches 141;
                                                       Synthetic.
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Patent No. 5856146
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MITSUGUNI, Hitoshi
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: RECAMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING SACCHARIDE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/505,377
FILING DATE: ("21-JUL.1995,
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 190128/1995
FILING DATE: ("21-JUL-1994,
PRIOR APPLICATION NUMBER: PP 109128/1995
FILING DATE: ("11-APR-1995,
PRIOR APPLICATION NUMBER: PP 109128/1995
FILING DATE: ("04-JUL-1994,
APPLICATION NUMBER: PP 109128/1995
FILING DATE: ("04-JUL-1995,
PRIOR APPLICATION NUMBER: DE DOGGNET NUMBER: PROGGNET NUMB
                US-09-346-237-1
US-09-514-302-4
US-09-514-599-2
US-09-514-599-2
US-09-313-677-2
US-09-313-677-2
US-09-313-677-2
US-09-313-677-19
US-09-313-677-19
US-08-474-140-11
US-08-474-140-11
US-08-474-545-11
US-08-478-331-11
US-08-996-333-11
US-08-996-333-11
US-08-996-333-11
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419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MITSUZUMI=1
TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 249688
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 556 amino acids
amino acid
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REGISTRATION NUMBER:
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MOLECULE TYPE: protein
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20004
  ADDRESSEE:
STREET: 41'
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TYPE: am
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JS-08-505-377-1
                                                                                                                                                   (without alignments)
541.277 Million cell updates/sec
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Sequence 1, Appli
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Sequence 2, Appli
Sequence 2, Appli
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Sequence 15,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-607-321-12
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Listing first 45 summaries

    protein search, using sw model

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Match Length DB
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Perfect score:
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APPLICANT: MITSUZUMI, HITOSHI
APPLICANT: KUBOTA, MICHI
APPLICANT: KUBOTA, MICHI
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING SACCHARIDE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                     1 MFSFGGNIEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYI 60
                                                                                                                                                                                                       RGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEY
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                               556;
                               Length
                                                  Indels
                            Score 2954; DB 2;
Pred. No. 1.1e-280;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
                                                 0; Mismatches
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APPLICATION NUMBER: US/08/798, 269
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Patent No. 6027918
                            100.0%;
100.0%;
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                                                 Matches 556; Conservative
                                       Similarity
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US-08-505-377-1
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                            Query Match
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100.0%; Pred. No. 1.1e-280;
tive 0; Mismatches 0;
                            FILING DATE: 21-JUL-1995
APPLICATION NUMBER: JF 190180/1994
FILING DATE: 21-JUL-1994
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: JF 109128/1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION NUMBER: JF NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         MITSUZUMI-1
                   US/08/505,377
                                                                                                                                                                                                                         25,618
                                                                                                                                                                                                       NAME: Browdy, Roger L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       TELEPHONE: (202) 628-5197
TELEFAX: 24968
TELEX: 24968
INFORMATION FOR SEQ ID NO: 1:
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amino acid
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LENGTH: 556 amino acid
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PRIOR APPLICATION DATA
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Best Local Similarity
Matches 556; Conserv
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181 RGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEY 240
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                                                                                       APPLICANT: MITSUZUMI, Hitoshi
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, TOSHIJUKI
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING 5
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Pred. No. 1.1e-280;
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/505,377
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 109128/1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP NOT YET RECEIVED APPLICATION NUMBER: JP NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                  Sequence 1, Application US/09055210 Patent No. 6346394 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Browdy, Roger L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MIT
TELECOMMUNICATION INFORMATION:
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100.0%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 628-519
(202) 737-3528
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amino acid
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Best Local Similarity 100.
Matches 556; Conservative
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                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                   .COMPUTER:
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                                                                                                                                                                                                                                              COUNTRY:
                                      -09-055-210-1
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APPLICANT: KONDO, KEIJI
APPLICANT: MIURA, YUTAKA
TITLE OF INVENTION: RAAF
TITLE OF INVENTION: SAME
FILE REFERENCE: 049441/0118
CURRENT APPLICATION NUMBER: US/09/242,690A
CURRENT FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: PCT/JP97/02924
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1996-08-22
PRIOR PILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
420
                                                                                                                                                                                               TNPFFFFSDFSDFVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYKQLI 480
                                                                                                                                                                                                                                                                                                                                                  NIRKRYNNCKRVKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNLLIGIGFPKKLKK 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                         GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYE
                                                                                                                                                                                                                                                                                                                                                                      301 IDAOWVDDFHHAVHAFITKEKDYYYODFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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protein
  ; MOLECULE TYPE:
US-08-399-646-2
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| 527 EFDD 530
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APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kelji
APPLICANT: TSUSAKI, Kelji
APPLICANT: HYTORI, Kazuko
APPLICANT: HYTORI, Kazuko
APPLICANT: HYTORI, Kazuko
APPLICANT: HYTORI, Kazuko
APPLICANT: SUGIMOTO, TOSHIYUKi
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            359
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                                                                                                                                                                               361
                                                     FKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKIV--KDDCGY
                                                                                                                            KIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAP
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
ATION APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATIONEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08399646
Patent No. 5556781
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MEDIUM TYPE: Floppy disk
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY:
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COUNTRY:
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US-08-399-646-2
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APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENOODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                   EIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDL-----IIYELHVGTFSQ 115
                                                                                                                                                                                                                                                                               EGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKIV--KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 YSRYRGRTHGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
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                                                  Gaps
                                                                                             13 GIFKLWAPYVNSVKLKLSKKLIPMEKN-----DEGFFEVEIDDIEENLTYSYIIE-DKR 65
                                                                                                                        NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGK-----FVIAESDLND
                                                  90;
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    Length 589;
                                                  Indels
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32.8%; Score 969; DB 1; I
39.5%; Pred. No. 3.2e-86;
iive 74; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Seventh Street, N.W., Suite 300 STATE: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compariable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08607321
Patent No. 5716813
GENERAL INFORMATION:
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                                                  Conservative
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ADDRESSEE: BROWDY AN
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  Query Match
Best Local Similarity
Matches 215; Conserv
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USA
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APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOSHİYUKİ
TITLE OF INVENTION: DNA ENCOLING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 PLPDPRTRRQPEGVH---ALSRT----FDPGAHRWQDAGWGRELQGSVIXELHIGTFTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GIFKLWAPYVNSVKLKLSKKLIPMEKN-----DEGFFEVEIDDIEENLTYSYIIE-DKR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 EIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDL------IIYELHVGTFSQ
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: FLOPPY disk
COMPUTER: TEMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,240
FILING DATE: 30-OCT-1997
CLASSIFICATION NUMBER: US 08/399,646
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: US 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTONEY/AGENT INPOMBATION:
NAME: REMAINT NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTONEY/AGENT INPOMBATION:
NAME: MANNY PORGET I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Mismatches 195;
                                                                                                                                                                                                                                                                 E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 969;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KUBOTA=5
                                                 Sequence 2, Application US/08961240 Patent No. 5830715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25,618
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TELECOMMUNICATION INFORMATION:
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39.5%;
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amino acid
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202-737-3528
                                                                                                             Michio
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Best Local Similarity 39.58
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-961-240-2
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                         GENERAL INFORMATION:
APPLICANT: KUBOTA
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                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                   JS-08-961-240-2
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.8%; Score 969; DB 1; Best Local Similarity 39.5%; Pred. No. 3.2e-86; Matches 215; Conservative 74; Mismatches 195
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY, AGENT INFORMATION:
           MBER: US/08/607,321
26-FEB-1996
                                                                                                                                                                                                                                                                                     KUBOTA=5
                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/POCKET NUMBER: KUBG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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                                                     CLASSIFICATION:
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EFDD 530
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amino acid

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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-605-501-2
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APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGINOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NOMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                241 DNVAMMLRDYRVDGLRLDAVHALKDERAVHILEEFGALADALSSEGGRPLTLIAESDLNN 300
                                                                                      348 YSRYRGRTHGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                         SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA 458
                                                                  PKIV---KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK
                                                                                                                                                                                                                                                                             FLKSKLSWK----IDEEVLDYYKQLINIRKRYNNCKRVKEVRREGNCITLIMEKIGIIA
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,501
FILING DATE: 26-FEB-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08605501
Patent No. 5834287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 59840 FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BROWDY, Roger L.
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APPLICANT: KUBOTA,
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APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SIGIMOTO, TOSHIYUKI
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
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                                                                                                                                                                                                                                                                                    116 EGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLV 175
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                                                    Gaps
                                                                                                                            13 GIFKLWAPYVNSVKLKLSKKLIPMEKN-----DEGPFEVEIDDIEENLTYSYIIE-DKR 65
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                                                    Indels
; Score 969; DB 2; L;
; Pred. No. 3.2e-86;
74; Mismatches 195;
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08399646 Patent No. 5556781 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
  32.8%;
  Query Match 32.8% Best Local Similarity 39.5% Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DATE OF INVENTION: EN NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 EFDD 530
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TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL 235
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39.5%; Pred. No. 3.2e-86;
iive 74; Mismatches 195;
                                                                                                                                                                                                                                                                  3: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION 1939
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: JP 59834
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUBOTA-5
                                                    Sequence 12, Application US/08607321 Patent No. 5716813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                      APPLICANT: KUBOTA, Michio APPLICANT: TSUSAKI, Keiji HAPLICANT: HATTORI, Kazuko APPLICANT: encreant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.8%
Best Local Similarity 39.5%
Matches 215; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   20004
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                                    US-08-607-321-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 YSRYRGRTHGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
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                  PatentIn Release #1.0, Version #1.30
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39.5%; Pred. No. 3.2e-86;
iive 74; Mismatches 195;
                          SOFTWARE: FEACHLIN RELEASE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UF 59834
FILING DATE: 07-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UF 59840
FILING DATE: 07-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: KUBOTA-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
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                                                                                                                                                                                                                                                                                                                                                                                                                             596 amino acids
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Matches 215; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Patent No. 5830715

GENERAL INFORMATION:
APPLICANT: KUDOTA, Michio
APPLICANT: HATORI, Keiji
APPLICANT: HATORI, Kazuko
TITLE OF INVENTION: ENZYME, ENGODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORWANT, AND THEIR PREPARATIONS AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE D.C.
                                                    :|| | : :::||||||||||: | | ||:| | | 307
                                                                                                                                                                 348 YSRYRGRTHGAPV -- GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                       406 SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNOM------IDPQSEEA 458
                                                                                                                                                                                                                                                                                                                                                                                     459 FLKSKLSWK----IDEEVLDYYKQLINIRKRYNNCKRVKEVRREGNCITLIMEKIGIIA 513
                       ENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGK-----FVIAESDLND 289
                                                                                                                               290 PKIV--KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,240
FILING DATE: 07-MAR-1997
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: US 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATFORDER: NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATFORDER: MARR-1994
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUI
TELECOMMUNICATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-3528 :
TELEX: 248633 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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Patent No. 5834287
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                               66 EIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDL------IIYELHVGTFSQ 115
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                                                                                                                                                                                                                       13 GIFKLWAPYVNSVKLKLSKKLIPMEKN-----DEGFFEVEIDDIEENLTYSYIIE-DKR 65
                                                                                                                                                                                                                                                      SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA
                                                                                                                                                                             60;
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                                                                                                                                                                          Indels
                                                                                                                           32.8%; Score 969; DB 2; L
39.5%; Pred. No. 3.2e-86;
iive 74; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                        Matches 215; Conservative
; TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-240-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                Query Match
Best Local Similarity
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Sequence 4, Application US/08399646
Patent No. 5556781
GENERAL INFORMATION:
APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 PDPASRYQPLGVHDKSQLI-RTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 FKLWAPYVNSVKLKLSKKLIPMEK-----NDEGFFEVEIDDIEENLTYSYIIE-DKREI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 GKLDYLAGLGVDFIELLPVNAFNGTHNWGYDGVQWFAVHEAYGGPEAYQRFVDAAHAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.5%; Score 959; DB 1; Length 597
40.2%; Pred. No. 3.1e-85;
ive 81; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                 E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUBOTA=5
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APPLICATION NUMBER: US/08/399,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 59840 FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 597 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 40.2%
Matches 202; Conservative
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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  534 EFDD 537
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                                                              RESULT 13
US-08-399-646-4
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                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSRYRGRIHGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 EIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDL~~~~~IIYELHVGTFSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 EGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKIV--KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GIFKLWAPYVNSVKLKLSKKLIPMEKN-----DEGFFEVEIDDIEENLTYSYIIE-DKR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GRFDIWAPEAGTVTLLAGGERYEMGRRPGNGPADEGWWTAADAPTGADVDYGYLLDGDEI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLKSKLSWK-----IDEEVLDYYKQLINIRKRYNNCKRVKEVRREGNCITLIMEKIGIIA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 969; DB 2; L.; Pred. No. 3.2e-86; 74; Mismatches 195;
                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 105 08/399,646
FILING DATE: 07-MAR-1994
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: XUBOTA-5
TELEPHONE: 202-628-5197
                                                            US/08/605,501
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39.5%;
                                                                               26-FEB-1996
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Best Local Similarity 39.5%
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 596 amino acids
amino acid
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-605-501-12
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                                                                                 FILING DATE:
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APPLICANT: KGDGTA, Michio
APPLICANT: TGUSKI, Keiji
APPLICANT: TGUSKI, Keiji
APPLICANT: TGUSKI, Kazuko
APPLICANT: TGUSKI, Kazuko
APPLICANT: SUGINOTO, TOShiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
NUMBER OF SEQUENCES: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADD
                                                               TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV-----IAESDLNDPKIV--KD 295
                                                                                                                                                                                                                                           296 DCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSW 466
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COMPUTER: IBM PC compatible
COMPUTER: PLOPPY disk
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB.1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: O7-MR-1995
FILING DATE: US-MR-1995
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FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 AEAAEGDHARLLELYRSLTALRR 519
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Patent No. 5716813
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 KIDEE-----VLDYYKQLINIRK 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein

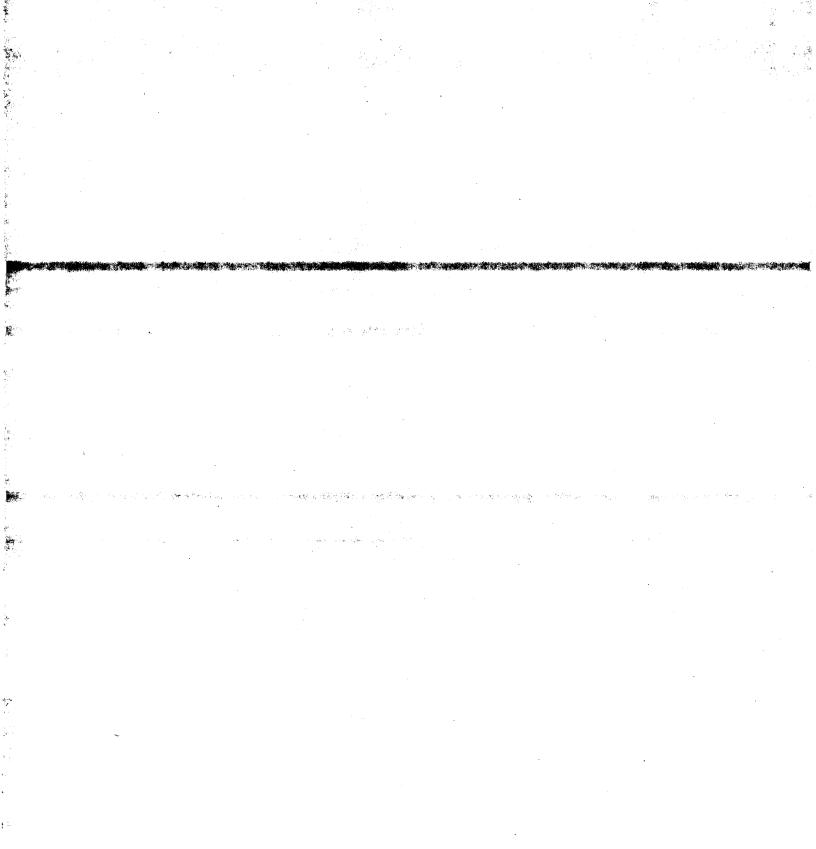
US-08-607-321-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-607-321-4
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APPLICANT: KUBOTA, Michic
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOShiyuki
APPLICANT: SUGIMOTO, TOShiyuki
"TTIE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
"TTIE OF INVENTION: TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                             PDPASRYQPLGVHDKSQLI-RTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVI 123
                                                                                                                                                                                                          124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI 183
                                                                                                                                                                                                                                                                               184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK 243
                                                                                                                                                                                                                                                                                                                                                   244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV----IAESDLNDPKIV--KD 295
                                                                                                                                                                                                                                                                                                                                                                                                                     DCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRT 355
                                                                                                    18 YDVWAPNAESVTLLAGGERYAMORRAETGPEDAGWWTAAGAPTDGNVDYGYLLDGDETPL 77
                                                                     15 FKLWAPYVNSVKLKLSKKLIPMEK-----NDEGFFEVEIDDIEENLTYSYIIE-DKREI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSW
                                   34;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                   Mismatches 186;
 Score 959; DB 1;
Pred. No. 3.1e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,240
FILING DATE: 30-0CT-1997
FLIANG DATE: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08961240 Patent No. 5830715 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 KIDEE-----VLDYYKQLINIRK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 AEAAEGDHARLLELYRSLTALRR 519
                                   81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
32.5%;
40.2%;
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Sever CITY: Washington STATE: D.C.
                   Similarity
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                                   Matches 202;
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   Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.5%; Score 959; DB 2; Length 597; Best Local Similarity 40.2%; Pred. No. 3.1e-85; Matches 202; Conservative 81; Mismatches 186; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV----IAESDLNDPKIV--KD 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 FKLWAPYVNSVKLKLSKKLIPMEK-----NDEGFFEVEIDDIEENLTYSYIIE-DKREI 67
                                                                                                                                                                                            KUBOTA=5
             APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTONREY, FAGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: XIBOTP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 KIDEE-----VLDYYKQLINIRK 484
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07-MAR-1995
JMBER: JP 59834
                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-240-4
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Search completed: July 15, 2002, 12:18:05 Job time: 97 sec



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July 15, 2002, 12:18:43 ; Search time 32.43 Seconds (without alignments) 1647.415 Million cell updates/sec
                                                                                                                                                                                                                                 1 MFSFGGNIEKNKGIFKLWAP......KLKKDELIKVNRGVGVYQLE 556
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            protein - protein search, using sw model
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                    US-09-298-924-8
2954
                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pirl:* pir2:* pir3:* pir4:*

PIR_71:*

Database

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Gaps

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Length 556; Indels 0

		alpha-amylase (EC	amylase (-amylase (_			malto-oligosyltreh	probable hydrolase					probable 1,4-alpha		hypothetical prote	1,4-alpha-qlucan b	1,4-alpha-qlucan b	qlycogen operon pr	alkaline amylopull	alpha-amylase (EC	pullulanase amyX -	1,4-alpha-qlucan b	pullulanase - Ther	glycogen operon pr	alpha-amylase (EC		1,4-alpha-glucan b	1.4-alpha-alucan h
SUMMARIES		32	87	35	27	97	70	27	73	63	75	16	94	01	34	15	39	66	94	31	02	85	39	04	88	12	48	00	29
ß	ΩI	JC513	S73087	JC5135	AH1827	JC4697	S6577	JC7727	AI0673	G707	G83375	H755	AG3194	D96001	S19134	AH1915	B56639	S185	S77094	E95031	G97902	G69585	S31839	H72204	S73088	S01312	S40048	E98000	69512
	DB	7	7	7	~	7	7	~	~	N	~	7	~	~	7	7	7	7	~	~	7	~	~	7	7	~	~	7	7
	Length	556	561	558	620	296	598	575	594	280	583	9	595	601	552	552	999	638	707	1280	1256	718	422	843	718	562	627	642	642
ø	Query Match	100.0	60.4	59.3	41.0	32.8	32.5	31.7		29.3	29.3	28.3	26.9		16.7	16.7	11.9		11.3		11.2		10.9	•	10.8	10.7	10.6		10.5
	Score	2954	1784.5	1748.5	1212.5	696	959	936	900.5	866.5	865.5	835.5	793.5	792.5	493	493	353	342.5	333.5			326	322.5	320	319.5	_	313.5	ij.	310.5
	Result No.			m			9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28

WFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKIVKDDCGYK 300

IDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPV 360

301

301

probable glycogen

2 E71565

999

10.4

306.5

29

241

GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYE 420

GVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHK 180

IEDKREIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDLIIYELHVGTFSQEGNFK 120

61 61 121

100.0%; Score 2954; DB 2; ilarity 100.0%; Pred. No. 2.3e-194; Conservative 0; Mismatches 0;

Best Local Similarity Matches 556; Conserv

Query Match

120

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0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	783 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		3 664 2 783 664 0 818 0 818 0 630 0 630 0 789 9 717 1073 1073 1073 7 70 7 70 7 70 7 70 7 70 7 70 7 70 7	4484800022800000	B86539 B72084 B8423 S84623 T0231 D70231 D7053 T01321 H84557 A44157 A44157 C97229 C97229 S34218 S34218 S34218 S34218 S34218 S34218		glycogen hydrolase glycosyl hydrolase probable isoamylas probable isoamylas l,4-alpha-glucan b glycosyl hydrolase glycosyl hydrolase pullulanase amyx { probable branching pullulanase [impor l
RESULT JC5132 JC5132 JAPha-amylase (EC 3.2.1.1) - Sulfolobus N,Alternate names: glycogenase C; Species: Sulfolobus acidocaldarius C; Date: 31-Jan-1997 #sequence_revision C; Accession: JC5132 R; Kobayashi, K.; Kato, M.; Miura, Y.; K Biosci. Biotechnol. Biochem. 60, 1720-1 A; Reference number: JC5131; MUID:971413 A; Reters preliminary; nucleic acid seq A; Molecule type: DNA A; Residues: 1-556 «KOB> A; Residues: 1-556 «KOB> A; Experimental source: strain ATCC33909 C; Comment: This enzyme hydrolyzes glyco C; Superfamily: trehalose trehalohydrola C; Reywords: glycosidase; hydrolase	1 lase () lasse () lasse Sulf lon: Jon: lon: Jo loce on lon: Jo loce on lon: Jo loce on lon: Jo loce on lon: Jo loce on loce o	es: 9 es: 9 es: 9 1997 1997 5132 foor: 6 enzy treba	2.1.1) 1ycogen 1 ycogen 2 ycogen #sequen 0, M.; Blochem is of t JC5131; y; nucl OB> DDBJ:D6 e: stra lose tr ase; hydra	- Sul ase calda calda Miura Miura Miura Muli Muli 4131; in A13 in A13 colyze	RESULT JUSTIA JUSTIA JUSTIA JUSTIA JUSTIA NA Lternate names: glycogenase C:Species: Sulfolobus acidocaldarius C:Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 C:Accession: JC51397 #sequence_revision 27-Feb-1997 C:Accession: JC5139 #sequence_revision 27-Feb-1997 R:KObpashi, K.; Kato, M.; Miura, Y.; Kettoku, M.; Biosci. Biotechnol. Biochem. 60, 1720-1723, 1996 A;Title: Gene analysis of trehalose-producing enzyn A;Reference number: JC5131; MUID:97141330 A;Residues: 1-556 «KOB> A;Cross-references: DbBJ:D64131; NID:9887704; PIDNI A;Experimental source: strain ATCC33909 C:Comment: This enzyme hydrolyzes glycosyltrehalose C:Superfamily: trehalose trehalohydrolase C;Keywords: glycosidase; hydrolase	RESULT Judya-amplase (EC 3.2.1.1) - Sulfolobus acidocaldarius Alpha-amplase (EC 3.2.1.1) - Sulfolobus acidocaldarius All ternate names: glycogenase C. Species: Sulfolobus acidocaldarius C. Species: Sulfolobus acidocaldarius C. Species: Jan-1937 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 C. Chate: 31-Jan-1937 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 C. Chate: Jan-1937 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 R. Kobayashi, K.; Kato, R. Kobayashi, K.; Kato, R. Kobayashi, K.; Kato, R. Kobayashi, K.; Kato, R. Kobayashi, K.; Kato, R. Kobayashi, M.; Komeda, T.; Iwamatsu, A. R. Kobayashi, M.; Komeda, T.; Iwamatsu, A. R. Kobayashi, M.; Komeda, T.; Iwamatsu, A. R. Kobayashi, M.; Komeda, T.; Iwamatsu, A. R. Kobayashi, M.; Komeda, T.; Iwamatsu, A. R. Katous: preliminary: nucleic acid sequence not shown A. Kosesion: JC513; A. Koseywords: JD513; A. Kosperimental source: strain ATCC33909 C. Comment: This enzyme hydrolyzes glycosyltrehalose to liberate trehalose. C. Superfamily: trehalose trehalohydrolase C. Superfamily: trehalose trehalohydrolase	RESULT 1 JUSTIA anylase (EC 3.2.1.1) - Sulfolobus acidocaldarius Allernate names: glycogenase Silfernate names: glycogenase Silfernate names: glycogenase Silfernate names: glycogenase Silfernate names: glycogenase C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Species: Sulfolobus acidocaldarius C:Superfamila : Solia : Millor: Solia : Solia : Millor: Solia : Solia : Millor: Solia : Solia : Millor: Solia : Solia : Millor: Solia :

ΩD	361 GDLPPRKEVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLJFMGEEYYE 420	Qy 478 QLINIRKRYN-NCKRVKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNLLIGIGF 534
ογ	421 TNPFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEFVLDYYKQLI 480	
QQ	421 TNPFFFFSDFSDPVLKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYRQLI 480	Qy 535 PKKLKKDELIKVNRGVGVYQL 555
oy Oy	481 NIRKRYNNCKRVKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNLLIGIGFPKKLKK 540 	342
Qy Dp	541 DELIKVNRGVGVYQLE 556 	RESULT 3 JC5135 alpha-amylase (EC 3.2.1.1) - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus
RESULT S73087	Sulfolobus solfatarious	C:Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 C:Accession: 155135 R:Kobayashi, K.; Kato, M.; Miura, Y.; Kettoku, M.; Komeda, T.; Iwamatsu, A. B:Accession: Biotechnol. Biochem. 60, 1882-1885, 1996 Biosci. Biotechnol. Biochem. 60, 1882-1885, 1996 Biotechnol. Biochem. 60, 1882-1885, 1996 Biotechnol. Biotechnol. Fire and a provession of new translance from the hune
N; Al C; Sp C; Da	24-Oct-1997 #text_change 20-Jun-2000	A; Reference number: JC5134; MUID:97141610 A; Accession: JC5135 A; Status: preliminary
C; Ac R; Se Mol.	an, C.C.Y.; Liu, Q.Y.; Penny, S.	A;Molecule type: DNA A;Residues: 1-558 <kob> A;Cross-references: DDBJ:D64130; NID:g987702; PIDN:BAA11010.1; PID:g1838936</kob>
A; T1 A; Re A; Ac	nation content of an archaeal genome: l	A;Experimental source: strain KM1 C;Comment: This enzyme hydrolyzes starch alpha-1,4 linkage adjacent to the alpha-1,1 C;Superfamily: trehalose trehalohydrolase
A;St A;MO		C; Keywords: glycosidase; hydrolase
A; Re A; Cr A; Ex	A;Residues: 1-561 <srn> A;Cross-references: EMBL:Y08256; NID:g1707679; PIDN:CAA69503.1; PID:g1707699 A;Experimental source: strain P2</srn>	Query Match 59.2%; Score 1748.5; DB 2; Length 558; Rest Local Similarity 58.9%; Pred No. 6 9c-112;
A; No C; Su	te: the nucleotide sequence was submitted to the EMBL Data Library, September 1996 perfamily: trehalose trehalohydrolase	nes 329;
C; Ke	ywords: glycosidase; hydrolase	Qy 3 SFGGNIEKNKGIFKLWAPYVNSVKLK-LSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII 61 1
Ou Be Ma	Query Match 60.4%; Score 1784.5; DB 2; Length 561; Best Local Similarity 59.2%; Pred. No. 2.4e-114; Matches 332; Conservative 90; Mismatches 130; Indels 9; Gaps 6;	62 EDKREIPDPASKYQPLGVHDKSQLIRTDYQILDLGKVKIEDLIIYELHVGTFSQEGNFKG
ð 8	3 SFGGNIEKNKGIFKLWAPYVNSVKLK-LSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII 61 : ::: :: : :: 2 TFGYKLDFNGVTFNIAMAPYORKYKIKTINRGIYEMERDDKGYFFTTIJNUVRUGDRYKYTI. 61	DD 61 DDASEIPDPASRYQPEGVHGPSQIIQESKEFNNETFLKKEDLIIYEIHVGTFTPEGTFEG 120 Qy 122 VIEKLDYLKDLGIIGIELMPVAQFPGNRDMGYDGVFLYAVQNTYGGPWELAKLVNEAHKR 181
ò	EDKREIPDPASRYOPIGYHDKSOLIRTPYOILDLGKYKIEDLIIVEIHVGTESORGNF	Db 121 VIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKK 180
2 A	DDNSEVPDPASRYQPEGVHGYSEIISPDFEWDDENSVKVKREDLVIYELHIGTFTSEGTF	QY 182 GIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYW 241 :
oy B	120 KGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAH 179 	242 FKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKIVKDDCGY
Qy Dp	180 KRGIAVILDVVXNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVE 239 : : :: :	300 KIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVGKSKRRGKTHGAP
දු දු	240 YWFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKIVKDDC 297	301 NIDAQWVDDFHHSIHAYLIGERQGYYTDFGNLDDIVKSYKDVEVYDGKYSNFKKKTHGEF 360 VGDLPPRKEVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYY :
S G	298 GYKIDAQWUDDFHHAVHARITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHG 357	Db 361 VGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYG 420 Qy 420 ETNPFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYRQL 479
δλ	APVGDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEE	421 BENPFYFFSDFSDSKLIQGVREGRKKENGODTDPQDESTFNASKLSWKIDEEIFSFYKIL
ą	KSVGDLDGCKFVVYIQNHDQVGNRGGGERLIKLVDKESYKIAAALYILSPYIPMIFMGEE	OY 480 INIRKRYN-NOKRVREPREGROITLIMEKIGIIASFDDIVINSKITGHILGIIGFPK 536 1
ð 8 .	418 YYETNPPFFFSDFSDPVLIKGYREGRLKENNOMIDPQSEEAFLKSKLSKKIDEBVLDYYK 477 	QY 537 KLKKDELIKVNRGVGVYQL 555 2:::::::::::::::::::::::::::::::::

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RESULT 6
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maltooligosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)
C;Species: Arthrobacter sp.
A;Variety: strain Q36
C;Species: Arthrobacter sp.
A;Variety: strain Q36
C;Species: Arthrobacter sp.
B;Variety: strain Q36
C;Species: S65770
B;Variety: K:; Hattori, K:; Nakada, T:; Kubota, M.; Sugimoto, T:; Kurimoto, M.
Biochim. Biophys. Acta 1289; 10-13, 1996
A;Title: Cloning and sequencing of trehalose biosynthesis genes from Arthrobacter sh;Reference number: S65769; MUID:96195835
A;References: S65770
A;Status: preliminary
Biosci. Biotechnol. Biochem. 60, 717-720, 1996
A;Title: Cloning and sequencing of trehalose biosynthesis genes from Rhizobium & A;Title: Cloning and sequencing of trehalose biosynthesis genes from Rhizobium & A;Reference number: JC4696; MUID:96219094
A;Reference number: JC4697
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                                                                                                      alpha-amylase [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp. (strain PCC 7120)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AH1827
R;Kanacko, T.; NaKamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AH1827
A;Status: preliminary
A;Molecule type: DNA
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C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C;Accession: JC4697
R;Maruta, K.: Hattori, K.: Nakada, T.; Kubota, M.; Sugimoto, T.; Kurimoto, M.
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; Pred. No. 3.7e-75;
86; Mismatches 151; ]
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46.5%;
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Matches 235; Conservative
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Best Local Similarity
Matches 198; Conser
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A;Molecule type: DNA
A;Residues: 1-598 <MAR>
A;Cross-references: EMBL:D63343; NID:g1255444; PIDN:BAA09668.1; PID:g1255446
C;Superfamily: trehalose trehalohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 EKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV----IAESDLNDPKIV--KD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGAPV - GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSW 466
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19 YDVWAPNAESVTLLAGGERYAMQRRAETGPEDAGWWTAAGAPTDGNVDYGYLLDGDETPL 78
                                                                                                                                                                                                                                                           15 FKLWAPYVNSVKLKLSKKLIPMEK-----NDEGFFEVEIDDIEENLTYSYIIE-DKREI 67
                                                                                                                                                                                                              34;
                                                                                                                                                         Length 598
                                                                                                                                                   32.5%; Score 959; DB 2; Length 59
40.2%; Pred. No. 7.8e-58;
.ive 81; Mismatches 186; Indels
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                                                                                                                                                      Query Match
Best Local Similarity 40.2%
Matches 202; Conservative
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Keywords: glycosidase;
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Length 575;

DB 2;

31.7%; Score 936;

Query Match

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probable hydrolase STY1503 [imported] - Salmonella enterica subsp. enterica serovar Tprobable hydrolase STY1503 [imported] - Salmonella enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: A10673
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S; Moule, S; O'Gara, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A;Reference number: AB0502; PMID:1167608
                                           10;
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A;Molecule type: DNA
A;Residues: 1.594 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01762.1; PID:g16502610; GSPDB:GN00176
                                                                                                                                                                                        --KIEDLIIYELHVGTFS 114
                                                                                                                                                                                                                    115 QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKL 174
                                                                                                                                                                                                                                                                                                                    175 VNEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFI 234
                                                                                                                                                                                                                                                                                                                                                                                                               235 LENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIA----EKAHQLGK--FVIAESDLN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPKIVKDDC--GYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYSRYRGRTHGAPVG-DLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM------IDPQSEEA 458
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                                                                                        15 FKLWAPYVNSVKLKL--SKKLIPMEKNDEGFFEVE--IDDIEENLTYSYIIEDKREIPDP 70
                                                                                                                                        64
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                                                                                                                      54;
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                                             Indels
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                    Pred. No. 2.8e-56;
; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%; Score 900.5; DB 2;
38.9%; Pred. No. 7.8e-54;
Live 79; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 FLKSKLSWKIDEE-----VLDYYKQLINIRK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: STY1503
C;Superfamily: trehalose trehalohydrolase
                                                                                                                                                                                        71 ASRYQPLGVHDKSQLIRTDYQILDLGKV---
38.78; Fig. 82;
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Best Local Sim:
Matches 199;
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probable glycosyl hydrolase PA2164 [imported] - Pseudomonas aeruginosa (strain PA01) C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Species: Bseudomonas aeruginosa C.Species: Bseudomonas aeruginosa 31-Dec-2000 C.Accession: G83375 R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; L.; Landon, M.V. Nature 406, 959-964, 2000 A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID:20437337 A; Accession: G83375 A; Status: preliminary A; Residues: 1-583 ACTO> A; Status: preliminary A; Residues: 1-583 ACTO> A; Cross-references: GB:AE004643; GB:AE004091; NID:g9948178; PIDN:AAG05552.1; GSPDB:GN A; Experimental source: strain PA01 C; Genetics: A; Gene: PA2164 C; Superfamily: trehalose trehalohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 DGRPGVPDPASQFQPDGVHGHS-----QVLDHGTYAWRVDEWRGRPWHEAVIYELHVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 DLNDPKIVKDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGR-IEDIEKTFKDVFVY 344
                                                                                                                                                                                            297 CGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTH 356
                                                                                                                                                                                                                                                                                                       GAPV--GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFM 414
                                                                                                                                                                                                                                                                                                                                                                                                                         ---NNOMIDPOSEEAFLKSKLSWK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 EDKREIPDPASRYQPLGVHDKSQLIRTDYQILDLGKV--KIE------DLIIYELHVG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 TFSQEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWEL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                               299 GGYGITAQWNDDIHHAIHTAVSGERQGYYADFGSLATLAYTLRNGYFHAGTYSSFRRRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 FKIDGLRLDAVHAIFDNSPKHILQEIAEKAH----QLGK--FVIAESDLNDPKIV--KDD
                                                                                                                 67;
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; Pred. No. 1.9e-51;
89; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                         GEEYYETNPFFFFSDFSDPVLIKGVREGRLKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IDEEVLDYYKQLINIR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 EAGSGEHARLHRFYRDLIALR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.3%;
Best Local Similarity 38.2%;
Matches 199; Conservative 8
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987

A;Accession: G70763

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-580 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIA 184
                                                                                                              VILDVVYNHIGPEGNYLLGLGP-YFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK 243
                                                                                                                                                                                                                                                                                                                                       ::|||| ||: | |:| :||:|| ||: | 252 EYHLDGLRFDAIDQIEDSSARHVLVEIAQRIRE------DITDRPIHLTTEDSRNII 302
                                                                                                                                                                                                                                                                                                                                                                                                                   ---VKDDCGYK--IDAQWVDDFHHAVHAFITKEKDYYYQDFGRIED--IEKTFKDVFVYD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 SLHPRDQDGNAPLFTAEWNDDFHNAVHVFATGETQAYYNDFADAPEKHLARALAEGFAYQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNGERLSILTD-KTTYLMAATLYI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKE-----NNQMIDPQSEEAF 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LIRTDYQILDLGKVKIEDLIIYELHVGTFSQEGNFKGVIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                          TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKSKLSWKIDEEV----LDYYKQLINIRKRY 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::||::|
481 QRSKLNWKQQHSEEGKAWLAFTRELLLLRQKH 512
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es 187; Conserv
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Matches 187;
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20;

the cyanobacterium Anaba

56;

Gaps

16.7%; Score 493; DB 2; Length 552; 28.6%; Pred. No. 5.3e-26; .ive 76; Mismatches 142; Indels 178;

99 64

186 205 240

--GPEGNYLLGLG

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C;Species: Anabaena variabilis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S19134
C;Accession: S19134
F;Sato, N.
Plant Mol. Biol. 18, 165-170, 1992
A;Title: Cloning of a low-temperature-induced gene lti2 from the cyanobacter A;Reference number: S19133; MUID: 92119230
A;Reference number: S19134
A;Recession: S19134
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-552 <ART>
A;Residues: 1-552 <ART>
A;Residues: 1-552 <ART>
A;Cross-references: EMBL:X59279; NID: 939252; PIDN:CAA41970.1; PID: 939253
C;Superfamily: neopullulanase; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 QWVDVTDPYATDIDESSGKDNSIARIKDGEKIVDTYVWQHDDKPLPADHELVIYELHVGD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYFSDRYKTFWGLTFNFD--DRGCD--QVRKFILENVEYWFKTFKIDGLRLDAVHAIFDN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 R--EIPDPASR--YQPLGVHDKSQLIRTDYQILDLGKVKIED------LIIYELHVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FKLWAPYVNSVKLKLS---KKLIPMEKNDEGFFE--VEIDDIEENL----TYSYIIEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 FS-----QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTY
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.7%
Best Local Similarity 28.65
Matches 159; Conservative
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               C. Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C. Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C. Accession: D96001
R. Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc.
Natl. Accession: D96001
A. Title: The complete sequence of the 1,683 kb psymB megaplasmid from the N2-fixing endd A. Reference number: A95842; MUID:21396508; PMID:11481431
A. Accession: D96001
A. Status: preliminary
A. Molecule type: DNA
A. Resperimental source: Strain 1021, megaplasmid psymB
A. Resperimental source: Strain 1021, megaplasmid psymB
A. Experimental source: Strain 1021, megaplasmid psymB
A. Science 293, 668-672, 2001
A. Authors: Rahn, D.; Kalman, S.; Keating, D. H.; Kiss, E.; Komp, C.; Lelaure, hebalul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D. H.; Wong, K.; Yeh, K. A. Retence 19182, SMD21447
A. Science: 19182, SMD21447
A. Science: 19182, SMD21447
A. Science: 19182, SMD21447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 FKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 HKRGIAVILDVVYNHIGPEGNYLLGLGP-YFSDRYKTPWGLTFNFDDRGCDQVRKFILEN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 VEYWFKTFKIDGLRLDAVHAIFDNSPKHIL----QEIAEK-AHQLGKFVIAESDLNDPKI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKDDCGYKI--DAQWVDDFHHAVHAFITKEKDYYYQDF----GRIEDIEKTFKDVFVYD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 GKYSRYRGRTHGAPVGD---LPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 AKEDNF-----SPEGSRARVPPQGRVNFLQNHDQIGNRAFGERLASLLQEDSLRVLAAAM 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8%; Score 792.5; DB 2; 36.9%; Pred. No. 1.9e-46; ive 79; Mismatches 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: trehalose trehalohydrolase
          C;Species: Sinorhizobium meliloti
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Best Local Similarity
Matches 192; Conserv
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hypothetical protein al10875 [imported] - Anabaena sp. (strain PCC 7120)
bypothetical protein al10875 [imported] - Anabaena sp. (strain PCC 7120)
c; Species: Anabaena sp.
k; Mote: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
c; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
c; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
c; Accession: AH1915
B; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A; Filler Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A; Filerence number: AB1807; MUID:21595285; PMID:11759440
312
                                                              DEMHWIAQEAKKTAGAKPFYNVAEHIPETTSIINLDGP------MDGCWHDSFYHI 340
                                                                                                                                                                                                                                                                                                                                                                        418
                                                                                                                                                                                                                                                                             341 IKAHIC------GDTFDLE-NLKDVI--DPKRQGFLGATN-------VVNYL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                               424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 YETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSW-----KIDEEVL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SKIDWTLLGNDLNRSLF 451
262 SPKH-ILQEIAEKAHQLGKFVIAE-----SDLNDPKIVKDDCGYKIDAQWVDDFHHA
                                                                                                                                                                                  313 VHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 TNHDHDHIMVELGNR-----EIFHDEAFRRAKLGTAILMTAV-----GVPLIWMGEEF
                                                                                                                                                                                                                                                                                                                                                                        373 QNHD-----QVGNRGNGERLSILTDK-----TTYLMAATLYILSPYIPLIFMGEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KQQDQ----
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|DYHKGLIGLRK--NN 464
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probable alpha-glucanotransferase - Anabaena variabilis

14

RESULT S19134

A;Status: preliminary

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26;
A; Molecule type: DNA
A; Residues: 1-552 <KURA
A; Residues: 1-552 <KURA
A; Cross-references: GB:BA000019; PIDN:BAB72832.1; PID:g17130220; GSPDB:GN00179
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C; Genetics:
C; Genetics:
C; Superfamily: neopullulanase; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                67 QWVDVTDPYATDIDESSGKDNSIARIKDGEKIVDTYVWQHDDKPLPADHELVIYELHYGD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ------WGPEFNYEHYDENLETYPARKFIGDTVRYWVGEYHLDGIRYDAARQIANY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 SPKH-ILQEIAEKAHQLGKFVIAE-----SDLNDPKIVKDDCGYKIDAQWVDDFHHA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 DFMHWIAQEAKKTAGAKPFYNVAEHIPETTSIINLDGP------MDGCWHDSFYHT 340
                                                                                                                                                                                                                                                                                                                                                                                    65 R--EIPDPASR--YQPLGVHDKSQLIRTDYQILDLGKVKIED------LIIYELHVGT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 FS-----QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GGPWELAKLVNEAHKRGIAVILDVVYNHI---------GPEGNYLLGLG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 PYFSDRYKTPWGLTFNFD--DRGCD--QVRKFILENVEYWFKTFKIDGLRLDAVHAIFDN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 VHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFI 372
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                                                                                                                                                                                                                                                                                                                       15 FKLWAPYVNSVKLKLS---KKLIPMEKNDEGFFE--VEIDDIEENL-----TYSYIIEDK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 GEYKP-----
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|DYHKGLIGLRK--NN 464
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Search completed: July 15, 2002, 12:18:44 Job time: 136 sec

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Hydrolase, Glycosidase...
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SEQUENCE 596 AA; 652
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Copyright (c) 1993 - 2000 Comp
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GLGX_HAEIN
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TREZ_MYCTU
GLGB_BACCL
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PULA_THEMA
AMY2_DICTH
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TREZ_ARTRM
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GLGB_SYNP7
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                 bacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2.1.141) (MTHase) (4-

sp. M-11.";
Biosci. Biotechnol. Biochem. 60:717-720(1996).
-- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic linkage in 4-alpha-D-((1->4)-alpha-D-glucanosyl)(n) trehalose vield trehalose and alpha-(1->4)-D-glucan.
-- PATHWAY: Trehalose biosynthesis.
-- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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P38939
P29093
P29093
Q08047
Q02905
Q02906
Q02751
Q54796
P32818
P32818
P30752
P30292
                                                                                                                                                                                                                                                                                                                           32.8%; Score 969; DB 1; Length 596; 39.5%; Pred. No. 1e-60; Live 74; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium sp. (strain M-11).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium.
NCBI_TaxID=391;
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73EA80AE0534DDCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Maltooligosyl trehalose trehalohydrolase).
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APU_THEET
016G_BACSP
GLGB_MAIZE
AMYA_ASPAW
AMYB_ASPON
MALT_CANAL
DEXB_STRPN
                                                                                                                                                  AMYM_BACAD
GLGB_ECOLI
AMY_ASPSH
ISOA_FLASP
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InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
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Best Local Similarity 39.59
Matches 215; Conservative
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IPR004193; isoamylase_N.

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                                                                                                                                     188 DAAHAAGLGVIQDVVYNHLGPSGNYLPRYGPYLKHGEGNTWGDSVNLDGPGSDHVRQYIL 247
                                                                                                                                                                                                                                                                 PKIV--KDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGK 347
                                                                                                                                                                                                                                                                                                    PRLLYPRDVNGYGLAGOWSDDFHHAVHVNVSGETTGYYSDFDSLGALAKVLRDGFFHDGS 367
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Maruta K., Hattori K., Nakada T., Kubota M., Sugimoto T., Kurimoto
"Cloning and sequencing of trehalose biosynthesis genes from
Arthrobacter sp. Q36.";
Biochim. Biophys. Acta 1289:10-13(1966).
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic
linkage in 4-alpha-D-((1->4)-alpha-D-9lucanosyl)n trehalose to
yield trehalose and alpha-(1->4)-D-glucano.
-!- PATHMAY: Trehalose biosynthesis.
-!- PATHMAY: TRELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         EGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLV
                                                                                              176 NEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=1667;
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40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDPASRYQPLGVHDKSQLI-RTDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVI 123
                                                                                                                                                                                      Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) (MTHase) (4-
alpha-D-[(1->4)-alpha-D-glucano]trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase).
                                                                                                                                                                                                                            FKLWAPYVNSVKLKLSKKLIPMEK-----NDEGFFEVEIDDIEENLTYSYIIE-DKREI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto T., Maruta K., Watanabe H., Yamashita H., Kubota M., Fukuda S., Kurimoto M.; Fukuda S., Kurimoto M.; Trahalose producing operon treYZ from Arthrobacter ramosus S34."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic linkage in 4-alpha-D-{(1->4)-alpha-D-glucanosyl}(n) trehalose t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVILDVVYNHIGPEGNYLLGLGPXFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFV----IAESDLNDPKIV--KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGRPINFSAVHPAALVVCSQNHDQIGNRATGDRLSQTLPYGSLALAAVLTLTGPFTPMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGAPV - - GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNOM-----IDPOSEEAFLKSKLSW
                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter ramosus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.
                                                                                                                                              Length 598;
                                                                                                                                                                                      Indels
                                                             // SIMILARITY.
8B5C610AD3766947 CRC64;
                                                                                                                                         Score 959; DB 1; L
Pred. No. 5.1e-60;
; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520
                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 KIDEE-----VLDYYKOLINIRK 484
Pfam; PF00128; alpha-amylase; 1
Pfam; PF02922; isoamylase_N; 1.
                                                                                65831 MW;
                                                                                                                                            32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 AEAAEGDHARLLELYRSLTALRR
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                      Hydrolase; Glycosidase.
                                                                              598 AA;
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                    Matches 202;
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ID TREZ_ARTRM
                                                           ACT_SITE
SEQUENCE
                                                                                                                                              Match
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Best Local
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490 EASTGDHARLLELYKSLTALRREH 513
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SEQUENCE
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between 'the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPKIVKDDC--GYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 KYSRYRGRTHGAPVG-DLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYIL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEA 458
                                                                                                                                                                                                                                                                                                                                                                      ---KIEDLIIYELHVGTFS 114
                                                                                                                                                                                                                                                                                                                                                                                             65 RSLRQPRGVH-------ELGREFDPARYAWGDDGWRGRDLTGAVIYELHVGTFT 111
                                                                                                                                                                                                                                                                                                                                                                                                                       QEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                             112 PEGTLDSAIRRLDHLVRLGVDAVELLPVNAFNGTHGWGYDGVLWYAVHEPYGGPEAYORF 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 VDACHARGLAVVQDVVYNHLGPSGNHLPDFGPYLGSGAANTWGDALNLDGPLSDEVRRYI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIA----EKAHQLGK--FVIAESDLN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPFTPMLFMGEEWGARTPWQFFTSHPEPELGEATARGRIAEFARMGWDPAVVPDPQDPAT 471
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                   15 FKLWAPYVNSVKLKL.--SKKLIPMEKNDEGFFEVE--IDDIEENLTYSYIIEDKREIPDP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malto-oligosyltrehalose trehalohydrolase (EC'3.2.1.141) (MTHase) (4-alpha-D-[(1->4)-alpha-D-glucano]trehalose trehalohydrolase) (Maltooligosyl trehalose trehalohydrolase).
                                                                                                                                                                                                                                                                                                                                   VNEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFI
             Trehalose biosynthesis.
                                                                                                                                                                                                                                                                   31.7%; Score 936; DB 1; Length 575; 38.7%; Pred. No. 2e-58;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                BY SIMILARITY.
; 284A3F20207E228B CRC64;
                                                                                                                                                                                                                                                                                            82; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 trehalose and alpha-(1->4)-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 FLKSKLSWKIDEE-----VLDYYKQLINIRK 484
                                   KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    71 ASRYQPLGVHDKSQLIRTDYQILDLGKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB045141; BAB40766.1; -.
InterPro; IPR0000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase.
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                                                                                                                                                                                                                            63079 MW;
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                                                                                                                                                                                                                  250 2
575 AA;
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                              Best Local Simi
Matches 198;
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16-0CT-2001
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                                                                                                                                                                                                               ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      Kwon T., Kim C.H., Choi Y.D.;
"Maltooligosyl trehalose synthase/trehalohydrolase encode proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 NGYGLAGOWSDDFHTAVHVSVSGETTGYYSDFESLAVLAKVLKNGFLHDGSYSSFRGRHH 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 FKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQ-----LGKFVIAESDLNDPKIV--KDD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 CGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTH 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 DPASRYQPLGVHDKSQLIR-TDYQILD---LGKVKIEDLIIYELHVGTFSQEGNFKGVIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 KLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 VILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKT 244
                                                                                                                                                                                                                                                                                                                                                                   t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 FKLWAPYVNSVKLKLSKKLIPMEKND----EGFFEVEIDDIEENLTYSYIIE-DKREIP 68
                                            Actinomycetales; Micrococcineae; Brevibacteriaceae; Brevibacterium.
                                                                                                                                                                                                                                                                trehalose production in Brevibacterium helvolum.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATAINITE ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic
linkage in 4-alpha-D-[(1->4)-alpha-D-glucanosyl](n) trehalose
yield trehalose and alpha-(1->4)-D-glucan.
-!- PATHWAY: Trehalose blosynhesis.
-!- PATHWAY: TEABLONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 FDVWAPDVSSVVLVADGRQYPMQKKETAPGSEGWWTASDAPPNGDVDYGYLLDGNTTPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQM-----IDPQSEEAFLKSKLSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAPVGD -- LPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C282314B6E9BA029 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%; Score 890.5; DB 1;
39.1%; Pred. No. 3.2e-55;
ive 76; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF039919; AAB95369.1; -.
InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IDEEVLDYYKQLINIRKRY 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.19
Matches 197; Conservative
Brevibacterium helvolum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV.

STRAIN-H37RV.

STRAIN-H37RV.

STRAIN-H37RV.

MEDLINE-98295987. PubMed-9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Borles R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Rutter S., Seeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence...

In Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                              4-
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1->4)-D-glucosidic
linkage in 4-alpha-D-((1->4)-alpha-D-glucanosyl)(n) trehalose
yield trehalose and alpha-(1->4)-D-glucan
-!- PATHMAX: Trehalose blosynthesis.
-!- PATHMAX: Trehalose blosynthesis.
-!- SIMILARIY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                      3.2.1.141) (MTHase)
                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) (WTI
alpha-D-[(1->4)-alpha-D-glucano]trehalose trehalohydrolase)
(Maltooligosyl trehalose trehalohydrolase)
TREZ OR RV1562C OR MT1613 OR MTCX48.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // SIMILARITY.
506190468F44B862 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Glycosidase; Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY
                                                                                                                                        (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64076 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z74020; CAA98329.1;
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TubercuList; Rv1562c; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT1613;
                                                              TREZ_MYCTU
Q10769;
01-OCT-1996 (
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                                 FREZ_MYCTU
RESULT
                                                                                                       DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R B DDB R DDB R B DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R DDB R
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Score 866.5; DB 1; Length 580; Pred. No. 1.5e-53;

29.3%;

Query Match Best Local Similarity

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   11;
                                                                                                                                    63 ROPDGVHARSORWEPPGOFGAARTD---TGWPGRSVEGAVIYELHIGTFTTAGTFDAAIE 119
                                                                                                                                                                                       414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 VILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKT 244
                                                                                                                                                                                                                                                                                                                                                                     297 CGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTH 356
                                                                                                     YQPLGVHDKSQ------LIRTDYQILDLGKVKIEDLIIYELHVGTFSQEGNFKGVIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEEYYETNPFFFFSDFSDPVLIKGVREGRLKE-----NNQMIDPQSEEAFLKSKLSWK 467
 37; Gaps
                                 FKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYIIEDKREI-PDPASR 73
                                                                  FRVWAPKPALVRLDVNGAVHAMTRSADGWWHTTV-AAPADARYGYLLDDDPTVLPDPRSA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
"The glgB gene from the thermophile Bacillus caldolyticus encodes a
thermolabile branching enzyme.";
                                                                                                                                                                     KLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIA
                                                                                                                                                                                                                                                                                                                         245 FKIDGLRLDAVHAIFDNSPKHILQEIAEKAH----QLGK--FVIAESDLNDPKIV--KDD
                                                                                                                                                                                                                                                                                                                                                                                                                                       GAPV -- GDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Seq. 3:221-232(1992).
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83; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycogen.
-i- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=93208370; Pubmed=1296817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme.";
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479 EAGSGEHARLHRFYRDLIALR 499
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   Conservative
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Matches 187;
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glycogen.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKVKIEDLIIYELHVGTFSQ--EGNFKGVIEKLD----YLKDLGITGIELMPVAQFPGN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 YF----SDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAV----- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HAIFDNS-PKHILQEIAEK--AHQLGKFVIAESDLNDPKIVKD--DCG----YKIDA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNNDRLYENPYAVEFLRQLNEAVFAYDPNVWMIAEDSTDWPRVTAPTYDGGLGFNYKWNM 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :: : | : : | : : : | FRAHVIRGGGAVGTRFCVWAPHAREVRLVGSFNDWNGTNSPLTKVNDEGVWTIVVPENLE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                 FGGNIEKNKGI----FKLWAPYVNSVKL----KLSKKLIPMEK-NDEGFFEVEIDDIEE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---QLIRTDYQILD 94
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01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLGLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 PPRKFVVFIQNHDQVG-----NRGNG---ERLSILTDKTTYLMAATLYILSPYIPLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGSEFAQFDEWKFAEEL-DWVL---------FDFELHRKMDE---
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                                                                                                                                                                                   Glycosyltransferase
                                                                                                                                                                                                                                                                        1F64C31495BB1B6E CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Geobacillus.
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                                                                                                                                                                                                   BY SIMILARITY BY SIMILARITY
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                       or send an email to license@isb-sib.ch)
                                                                                                                                                                         Glycogen biosynthesis; Transferase; ACT SITE 309 309 BY SIMI ACT_SITE 352 352 BY SIMI ACT_SITE 420 420 BY SIMI SEQUENCE 666 AA; 78096 MW; 1F64C
                                                                                  Interpro; IPR000461; Alpha_amylase.
Interpro; IPR04193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                               EMBL; 214057; CAA78440.1; -
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Matches 142; Conserv
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P30538;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                   Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
"Molecular cloning and nucleotide sequence of the glycogen branching
enzyme gene (glgB) from Bacillus stearothermophilus and expression in
Escherichia coli and Bacillus subtilis.";
Mol. Gen. Genet. 230:136-144(1991).
-i- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 NLTYSYII--EDKREI--PDPASRYQPLGVHDKSQLIR-TDYQILD------LGKVKI 100
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                                                                                                                                                                                                                                                                                                                                                         -i- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS APPROXIMATELY 55 DEGREES CELSIUS.
-i- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 639;
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                                                                                                                                                                                                                                                                                                                               PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
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24.9%; Pred. No. 1.1e-16;
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InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
STRAIN=1503-4R;
MEDLINE=92079888; PubMed=1745226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase_N; 1.
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414 ILPFSHDEVVH-GKKSLLSKMPGTYEEKFAQLRLLYGYLLTHPGKKLLFMGGEFGQ---- 468
                    484
                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pullulanase precursor (EC 3.2.1.41) (Alpha-dextrin endo-1,6-alpha-glucosidase) (Pullulan 6-glucanohydrolase).
                   425 FFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYKQLINIRK
                                                                                                                                                                                                                                                                                             Bibel M., Brettl C., Gosslar U., Kriegshaeuser G., Liebl W.;
"Isolation and analysis of genes for amylolytic enzymes of the
hyperthermophilic bacterium Thermotoga maritima.";
FEMS Microbiol. Lett. 158:9-15(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics and the
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C42DDE233D54FE77 CRC64;
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                                                                                                                                                                                                                                Thermotogales; Thermotoga.
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InterPro: IPR004193; Isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; Isoamylase_N; 1.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-98115241; PubMed-9453151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ001087; CAA04522.1; -. EMBL; AE001821; AAD36907.1; -.
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                                                                                                                                                                                                                      Thermotoga maritima.
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"Cloning and expression in Escherichia coli of two additional amylase genes of a strictly anaerobic thermophile, Dictyoglomus thermophilum, and their nucleotide sequences with extremely low quantne-plus-cytosine contents.";
Eur. J. Biochem. 176:243-253(1988).
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01-APR-1990 (Rel. 14, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Alpha-amylase 2 (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
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                                                                                        88; Mismatches 185; Indels 194;
Length 843;
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                                              Pred. No. 6.3e-15
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Score 320;
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10.8%;
                                         23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 IIYELHVGTFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyoglomus thermophilum.
                                                                                             Conservative
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752 RLKNAEEIKK 761
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                                              Similarity
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                                                                                        Matches 143;
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P14898;
Query Match
Best Local 3
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ID AMY2_D
AC 01.4PR
DT 01.4PR
DT 01.5PR
DT 01.5PR
DE ALPha...
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degradation.
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                       GLGB_BACSU
P39118;
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ACT_SITE
SEQUENCE
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                                                                                           enzyme).
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                          24;
                                SUBCELLULAR LOCATION: Cytoplasmic.
MISCELLANEOUS: WHEN COMPARED TO AMYA, AMYB PRODUCED LARGER AMOUNTS
                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 AKLVNEAHKRGIAVILDVVYNHIG------PEGNYLLGLGPYFSDRYKTPWGL-- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 --TFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHA------IFDNSPK--- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 TKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 VGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYETNPFFFFSDFSDPVLIK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | | :: | | |:: | GNR--TLHEHARLPIPWSDD------KQDKELIDFYRQLVKIRKSHPALYKGTFIPI 499
                                                                                                                                                                                                                                                                                                                                                             7 NIEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYIIEDKRE 66
                                                                                                                                                                                                                       InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HILQEIAEKAHQLGKFVIAESDLNDPKIVKDDCGYKIDAQWVDDFHHAVHAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 PETFYFGEIVETPKETKKYVGKF-DGTLDFYLFKIIRD---FFIGKRW-----S
                                                       OF REDUCING SUGAR. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
PATHWAY: POLYSACCHARIDE DEGRADATION.
                                                                                                                                                                                                                                                                                                                                        Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 FSDMISFIKETQEESILVLINIEDKEEIFNLNGTYRDLFSGNIYTNSLKLG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NNCKRVKEVRREGNCITLIMEK----IGIIASFDDIVINSKITGNLLIG 531
                                                                                                                                                                                                                                                                                                                   DB 1; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYKQLINIRKRY----
                                                                                                                                                                                                                                                                                                                                                                                                         67 IPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDLIIYELHVGTFSQE--
                                                                                                                                                                                                                                                           SIMILARITY.
SIMILARITY.
9583342CFB7A369F CRC64;
                                                                                                                                                                                                                                                                                                                                        Mismatches 180;
                                                                                                                                                                                                                                                                                                                 10.7%; Score 315; DB 1; 21.7%; Pred. No. 8.3e-15;
                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                             KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                       ΒX
                                                                                                                                                                                                                                                                                                                                        Conservative 105;
                                                                                                                                                                                                                                                                                66999 MW;
                                                                                                                                                                                        EMBL; X13199; CAA31586.1; -.
                                                                                                                                                                                                    2; $01312.
                                                                                                                                                                                                                                                                                562 AA;
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Matches 128; Conserv
                                                                                                                                                                                                               Q08751; 1BV2
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ACT_SITE
SEQUENCE
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HSSP;
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셤
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 FGGNIEKNKG----IFKLWAPYVNSVKLK-----LSKKLIPMEKNDEGFFEVEIDDIEE 53
                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1.4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:3431-3441(1997).

-!- FUNCTION: CATALYSES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC LINKAGES IN GLYCOGEN BY SCISSION OF A 1,4-ALPHA-LINKED OLIGOSACCHARIDE FROM GROWING ALPHA-1,4-GLUCAN CHAINS AND THE SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOW EFFICIENT SPORULATION.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHATI,4-GLUCAN CHAINS.
CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiel J.A.K.W., Boels J.M., Beldman G., Venema G., "Glycogen in Bacillus subtilis: molecular characterization of operon encoding enzymes involved in glycogen biosynthesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycogen biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64B0A5553B6767BA CRC64;
                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 313.5; DB 1;
Pred. No. 1.2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS
627 AA.
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SIMILARITY.
SIMILARITY.
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Subtinist; BG10907; G1gB.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase.N.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94195107; PubMed=8145641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 11:203-218(1994)
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EMBL; AF008220; AAC00214.1; -.
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   STANDARD;
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352 3
420 4
627 AA;
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                                                                                                                                                                                                                              Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                              462
                                                                                     ILDLGKVKIEDLIIYELHVGTFSQEG-----NFKGVIEKL-DYLKDLGITGIELMPVAQF 145
                                                                                                    F---DNSPKH---ILQEIAEKAHQLGK-----FVIAESDLNDPKI--VKDDCG----YK 300
                                                                                                                                                                                                                                                          : |::| : | :| | 375 WNMGWMNDVLKYMET-PPEERRHCHQLISFSLLYAFSEHFVLPFSHDEVVYGKKSL---- 429
                                                                                                                                       PGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLG 203
                                                                                                                                                                                                                                                                                                                                            355 THGAPVGDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFM 414
                                                                                                                                                                                                                                                                                                                                                                     ----LNKMPGDYWQKFAQ------462
                                                                                                                                                                                                                                                                                                                                                                                                                                               KLSWKIDE----EVLDYY--KQLINIRKRYNNCKRVKEVRREGNCITLIMEKIGIIASF 515
                                                                                                                                                                                                                                                                                           301 IDAQWVDDFHHAVHAFITKEKDYYYQ--DFGRIEDIEKTFKDVFVYD----GKYSRYRGR 354
                                      91
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1-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
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NLTYSY-IIEDKREI---PDPASRYQPLGVH-------DKSQLIRTDYQ
                                                                                                                                                                                        LGPYFS----DRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHAI
                                                                                                                                                                                                                                                                                                                                                                                                             GEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQMID--PQSEEA------FLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces aureofaciens.
Bacteria: Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycogen.
PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
PATHWAY: MONOMER (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces aureofaciens.;
Biochim. Biophys. Acta 1200:334-336(1994).
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STRAIN-CCM 3239 / ATCC 10762;
MEDLINE-94347823; Pubmed-8068720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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551 TPVVYHQYDVG 561
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01-OCT-1996 (
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P52980;
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                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                               51 IEENLTYSYII---EDKREI-PDPASRYQPLGVHDKSQLIRTDYQILDL-----GKVKI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ED--LIIYELHVGTFSQEGNFKGVIEKLD-YLKDLGITGIELMPVAQFPGNRDWGYDGVF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 AQWVDDFHHAVHAFITKE---KDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAP 359
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           3 SFGGNIEKNKGI----FKLWAPYVNSVKLKLSKKL-----IPMEK-NDEGFFEVEIDD 50
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 TP-----WGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHAIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 296.5; DB 1; Length 764; 24.6%; Pred. No. 2.5e-13; ive 88; Mismatches 177; Indels 119
                                                                                                                                                                                                                                  Glycogen biosynthesis, Transferase, Glycosyltransferase.

ACT_SITE 440 440 BY SIMILARITY.

ACT_SITE 493 493 BY SIMILARITY.

ACT_SITE 761 851 BY SIMILARITY.

ERQUENCE 764 AA, 85325 MW, 684548284A268ACF CRC64;
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BY SIMILARITY.

6845482E4A268ACF CRC64;
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                                                                                                                                 EMBL, L11647, AAA67437.1; InterPro; IPR000461; Alpha_amylase. InterPro; IPR001899; Gram_pos_anchor. InterPro; IPR004193; isoamylase_N.
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                                                                                                                                                                                                     Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase_N; 1.
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GLGB OR SLL0158.
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Matches 125;
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TIGR; HI1358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 VYELHLGSWLHTAYDEPVKTLHGEGVPVEVSEWNTGARFLTYYELVDKLIPYVKELGYTH 311
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                                                          MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                 SUBUNIT: MONOMER (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%; Score 282; DB 1; Length 770; 28.9%; Pred. No. 2.6e-12; Live 46; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycogen biosynthesis; Transferase; Glycosyltransferase;
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Y SIMILARITY.
Y SIMILARITY.
A435AFCA7703FA8A CRC64;
  Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                            -! - PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D63999; BAA10073.1; -
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
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BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00128; alpha-amylase; 1
Pfam; PF02922; isoamylase_N; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.99
Matches 89; Conservative
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P45178;
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ACT_SITE
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GLGX_HAEIN
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 EQTY----PIFSQRGIDDQTYYWRNDQGRYINW--TGCGNMLNLSSDVGRKWVVDCLRY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 LOARGLONYWGYNPLAMFAVEPKYAATNNPLAEFKTMYKAFHKAGIEVILDVVFNHSAES 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 WVEQCHIDGFRFDLATVLGRDTPDF-----NSSAQLFTDIKNEPSLQNIKLIAEPWDIG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.K., Hanna M.C., Nguyen D.T., Sauddek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LILTHURGE AND THE PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/
-!- FUNCTION: THIS PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/
CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 DLIIYELHVGTFSQ------EGNFKGVIE--KLDYLKDLGITGIELMPV-----
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                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBL_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}.\ ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E2B71F610E8B1CAC CRC64;
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glycogen operon protein glgX (EC 3.2.1.-).
GLGX OR HI1358.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase_N; 1.
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14; Conservative
                                                                                                                                                                Haemophilus influenzae
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Tuberculist; Rv1326c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω.
                                                                                               ----SILTDKTTYLMAATL--YILSPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVR 440
                                                     435 NFITAHDGFTLKDLVSYNOKHNETNGEENRDGRNE-----NYSYNH---GVEGSTESL 484
375 HYGYQVGNFPSYFAEWNDRFRDDLCRFWLWKSGEIGAFAERFAGSSDLFKKNDRLPHTTL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s:
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Baddocok K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Caborne J., Oghorn T., Rajanfram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Rajanfram M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Seeger K., Skelton S., Barrell B.G.; Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                          Probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen
                               -----TFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNGERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycogen.
PATHRD STEP IN GLYCOGEN BIOSYNTHESIS.
SUBUNT: MONOMER (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages
                                                                                                                                                             EGRLKENNQMIDPQSEEAFLKSKLSW-KIDEEVLDYYKQLINIRKRYNNCKR
                                                                                                                     | : : | : | SEPQKSAVENNRTFAQSGLLMSLLLANGTPMLLAGDEFGNTQ-----
                                                                                                                                                                                                                                                                                                       (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                           731 AA
                                                                                                                                                                                                                                                                                                                                                                       branching enzyme).
GLGB OR RV1326C OR MTI368 OR MTCY130.11C.
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z73902; CAA98090.1; -.
EMBL; AE007010; AAK45632.1; -
TIGR; MT1368; -.
                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
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GLGB_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 SQEGNFKGVIEKL-DYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 FKLWAPYVNSVKL-----KLSKKLIPME-KNDEGFFEVEIDDIEENLTYSY-----II 61
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16-OCT-2001 (Rel. 40, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 FVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPY-----IPLIFMGEEY 418
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
MEDILINE-33216700; PubMed-8463281;
Thon V.J., Khalil M., Cannon J.F.;
"Isolation of human glycogen branching enzyme cDNAs by screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 273; DB 1; Length 731;
                                                                                                                                              Glycogen biosynthesis; Transferase; Glycosyltransferase; Complete proteome.

ACT_SITE 411 411 BY SIMILARITY.
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-> Q (IN REF. 2).
EE2BFEF765352617 CRC64;
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BY SIMILARITY
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
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                                                                                Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                         223
81729 MW;
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731 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                              -1- PATHWAY:
-1- SUBUNIT: MONOMER.
-1- SUBUNIT: MONOMER.
-1- SUBUNIT: MONOMER.
-1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN LIVER AND MUSCLE.
-1- DISEASE: DEFECTS IN GREL ARE THE CAUSE OF GLYCOGEN STORAGE DISEASE
-1- V (GSD-IV) (ALSO KNOWN AS ANDERSEN'S DISEASE); A RARE FORM OF GLYCOGENOSIS CHARACTERIZED BY THE ACCUMICATION OF ABNORMALLY
STRUCTURED GLYCOGEN THAT RESULTS IN EARLY ONSET HEPATIC CIRRHOSIS,
CARDIAC ARREST AND NUMBORNOSCULAR DISEASES. MOST CHILDREN WITH THIS
CONDITION DIE BEFORE TWO YEARS OF AGE. NO TREATMENT APART FROM
LIVER TRANSPLANTATION HAS BEEN FOUND TO PREVENT PROGRESSION OF THE
DISEASE.
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 TGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVV---- 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 SFGVHRCADGGLYSKEWAPGAEGVFLTGDFNGWNPFSYPYKKLDYGKWELYIPPKQNKSV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 LVPHGSKLKVVITSKSGEILYRISPWAKYVVREGDNVNYDWIHWD----PEHSYEFK--- 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ENLTYSYIIEDKREIPDPASRYQPLG 78
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9.1%; Score 270; DB 1; Length 702;
21.9%; Pred. No. 1.6e-11;
Live 90; Mismatches 202; Indels 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; I.
Pfam; PF02922; isoamylase, N. 1.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
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ACT_SITE 357 357
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nes 147; Conserv
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 RELATION DEPT.
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386 DEDALLTYLMLA-----NHLVHTLCPDSITIAEDVSGMPALCSPISQGGGGFDYRLAMAI 439
                                                        332 ED----IEKTFKDV-----FVYDGKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQVGNR 381
                                                                                                                                                                                                                                                                                                                                           537 N----FMGNEFGHPEWLDFPRKG----NN-----ESYHYARRQFHLTDDDLLRYKFL 580
                                                                                                                                                                                                                                                                                                                                                                                                 480 INIRKRYNNCKR------VKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNL 528
                                                                                      882 GNGERLSILTDKTT--YLMAATLY----ILSPYIPLI-------FMGEEYY
                                                                                                                                                                                                                                                                                     ETNPFFFFSDFSDPVLIKGVREGRLKENNOMIDPQSEEAFLKSKLSWKIDEEVLDYYKQL
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Search completed: July 15, 2002, 12:24:34 Job time: 386 sec

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ALIGNMENTS

Q97FP9 Q59832 Q9KY06 Q9KNE8

12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:*		TO	01-NOV-1996 01-NOV-1996 01-DEC-2001
		O D D	01-DEC-2001 ALPHA-AMYLAS TREZ.
		SO	Sulfolobus a
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Match Length UB ID	Description	RA G	Maruta K., M
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561 17	P95867 súlfolobus	RT	of trehalose
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559 1 0	Q9uwn9 sulfolobus	RL	Biochim. Bio
17	Q973h4 sulfolobus .	DR	EMBL; D64131
581 2 0	Q9adi5 streptomyce	DR	EMBL; D83245
583 16	Q9ilv1 pseudomonas	DR	InterPro; IP
600 16	Q9rx51 deinococcus	DR	InterPro; IP
16	Q92u63 rhizobium m	DR	InterPro; IP
217 17	Q973h5 sulfolobus	DR	Pfam; PF0012
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440 2	Q93q35 myxococcus	DR	PROSITE; PS0
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InterPro; IPR004193; isoamylase_N.
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RY STAIN-ATCC 35092 / DSM 1617 / P2;

RX MEDLINE-21332296; PubMed=11427726;

RA AWAYEZ M.J., Confalonieri F., Zivanovic Y., Allard G.,

RA AWAYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA AWAYEZ M.J., Erauso G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Thi-Ngoc H.P., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

"The complete Sci. U.S.A. 98:7835-7840(2001).
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                                  Gaps
                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-AMYLASE PRECURSOR (MALTO-OLIGOSYLTREHALOSE TREHALOHYDROLASE)
(TREZ) (EC 3.2.1.141).
                                                      MFSFGGNIEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYI
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             Length 556;
                                 Indels
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            Score 2954; DB 1;
Pred. No. 4.7e-189;
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Archaea; Crenarchaeota;
NCBI_TaxID=2287;
                      Similarity
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                                                                                                                                                                                                                                                        Kato M., Kettoku M., Miura Y., Komeda T., Konishi Y., Shindo K., Kobayashi K., Iwamatsu A.; The gene analysis of the new amylases from the hyper thermophilic archae Sulfolobus."; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    GYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHG
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Pred. No. 4.9e-111;
); Mismatches 130; Indels
Pfam: PF00128; alpha-amylase: 1.
Pfam: PF02922; isoamylase_N; 1.
Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 561 AA; 64370 MW; B00E403020F6B242 CRC64;
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Archaea; Crenarchaeota;
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Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase_N; 1.
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Weiting Y., Wei C., Hui W., Li L., Cheng J.;
"Maltoligosyl trehalose trehalohydrolase from Sulfolobus shibatae.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201335; AAFI7553.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|
VGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYKQL 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIRKRYN-NCKRVKEVRREGNCITLIMEKIGIIASFDDIVINSKITGNLLIGI--GFPK 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 IKMRKELSIACDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQ
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NCBI_TaxID=2286;
                                                                                                                                                                                                                       7;
                                                                                                                                                                                559;
                                                                                                                                                                         59.2%; Score 1748.5; DB 1; Length 58.9%; Pred. No. 1.2e-108; ive 87; Mismatches 136; Indels
                                                                                                            79FBE23A7CD38B4E CRC64;
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALTOOLIGOSYL TREHALOSE TREHALOHYDROLASE.
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EMBL; D64130; BAA11010.1; -.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase,1.
Pfam; PF02922; isoamylase_N; 1.
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InterPro; IPR004193; isoamylase_N.
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                                                                                      322; isoamylase_N; 1.
559 AA; 64790 MW; 7
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                                                                                                                                                                         Query Match (59.2)
Best Local Similarity 58.99
Matches 329; Conservative
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Sulfolobus shibatae.
                                                                                                            SEQUENCE
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PubMod=11572479;
PubMod=11572479;
Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
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                                                                                                                                                                                                                                                                                              122 VIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKR 181
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                                                                                                                                       SFGGNIEKNKGIFKLWAPYVNSVKLK-LSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 FKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGKFVIAESDLNDPKIV--KDDCGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDEEVLDYYKQL
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                                                           559;
                                                           Length
                                                                                                Indels
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Last sequence update)
Last annotation update)
                                                           DB 1;
                                                                                                141;
                                                     98; Score 1711.5; DB 1
08; Pred. No. 3.6e-106;
87; Mismatches 141;
8C0F0F38A5AE2846
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64619 MW;
                                                         57.9%;
58.0%;
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19,
                                                 Query Match
Best Local Similarity 58.09
Matches 324; Conservative
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Q973H4;
Q1-DEC-2001 (TTEMBLTE1 1:
Q1-DEC-2001 (TTEMBLTE1 1:
Q1-DEC-2001 (TTEMBLTE1 1:
PUTATIVE ALPHA-AMYLASE.
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559 AA;
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Pseudomonas
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 NSPKHILQEIAEKAHQLGKFVIAESDLNDPKIVKDDCGYKIDAQWVDDFHHAVHAFITKE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; ALS89708; CAC33923.1;
EMBL; ALS89708; CAC33923.1;
Pfant: PF00128; alpha-amylase.
Pfont: PF00128; alpha-amylase.
SEQUENCE 581 AA; 63952 MW; 8816DFF3BC1A3408 CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                        Length 359;
"Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain?.";
DNA Res. 8:123-140(2001);
EMBL; AP000984; BAB65939.1;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    11 protein; Complete proteome.
359 AA; 41600 MW; 4D9F429099E81665 CRC64;
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66.0%; Pred. No. 2.6e-78;
tive 53; Mismatches 66;
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MEDLINE-97000351; PubMed-8843436;
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Best Local Simil
Matches 235; (
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                                                                                                                       Gaps
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STRAIN-ATCC 15692 / PRO1;
MEDLINE-2043737 PubMed-10984043;
MEDLINE-2043737 PubMed-10984043;
Strover C.K., Pham X.-0.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Gollty L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Felger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                            184 AVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 TFKIDGLRLDAVHAIFDNSPKHILQEIAEKAHQLGK-----FVIAESDLNDPKIV--KD
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                                                                                                                 43;
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           Length 581;
                                                                                                                 Indels
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Score 942.5; DB 2;
Pred. No. 7.5e-55;
3; Mismatches 174;
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Nature 406:959-964(2000).
EMBL; AE004643; AAG05552.1; -.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
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                                                                                                                 Conservative
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01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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01-DEC-2001
                                                                                                     Query Match
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                                                                             20;
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                                                                                                                                              62 EDKREIPDPASRYQPLGVHDKSQLIRTDYQILDLGKV--KIE------DLIIYELHVG 111
                                                                                                                                                            112 TFSQEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWEL 171
                                                                                                                                                                                                     285
                                                                                                                                                                                                                                                                                            DDNRASLLRQ--GY--DAQWNDDGHHALHVLLTGENDGYYQDYPEPLRCLARCLAEGFVY 345
                                                                                                                                                                                                                                                                                                                                                                         DGKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYI 404
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                                                                             Gaps
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                                                                                                  4 FGGNIEKN-KGIFKLWAPYVNSVKLKLSK-KLIPMEKNDEGFFEVEIDDIEENLTYSYII 61
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Qitterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Flelschmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                               RKFILENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQEIAEKAH-----QLGKFVIAES
                                                                                                                                                                                                                                                                                                                             DENDPKIVKDDCGYKIDAQWVDDFHHAVHAFITKEKDYYYQDFGR-IEDIEKTFKDVFVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                             67;
                                                       Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genome sequence of the radioresistant bacterium Deinococcus
                                                                             Indels
                     651CD7A918833E00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALTOOLIGOSYLTREHALOSE TREHALDHYDROLASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQSEEAFLKSK-----LSWKIDEEVLDYYKQLINIRKRY 486
                                                       DB 16;
                                                      29.3%; Score 865.5; DB 16; 38.2%; Pred. No. 1e-49; iive 89; Mismatches 166;
PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
          Hydrolase; Complete proteome.
SEQUENCE 583 AA; 65657 MW;
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EMBL; AE001905; AAF10042.1;
                                                                 Best Local Similarity 38.2
Matches 199; Conservative
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                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 QPLGVHDKSQLI----RTDYQILDLGKVKIEDLIIYELHVGTFSQEGNFKGVIEKLDYLKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHIGPEGNYLLGLGP-YFSDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLDAVHAIFDNSPKHILQEIAEKAHQLG--KFVIAESDLNDPKIVKDDCGYKIDAQWVDD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 FHHAVHAFITKEKDYYYQDF-GRIEDIEKTFKDVFVYDGKYSRYRGRTH--GAPVGDLPP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 FHHETRVTLTGEQEGYYAGYRGGAEALAYTIRRGWRYEGQFWAVKGEEHERGHPSDALEA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.; "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 LGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVY 191
                                                                                                                                                                                                                                                                                                                                                                                         95
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                                                                                                                                                                                                                                                                                                                                                                           RKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYETNPFF
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                        191; Indels
                                                                                                                                                    594091EC093F8A44 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE 1,4-ALPHA-GLUCAN BRANCHING ENZYME PROTEIN
                                                                                                                                                                                                                               28.3%; Score 835.5; DB 16; 36.8%; Pred. No. 1.1e-47;
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                                                                                                                                                                                                                                                                                      89; Mismatches
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TIGR; DR0464; –
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
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STRAIN=1021;
MEDLINE=21396508; Pubmed=11481431;
                                                                  pfam; Pr00128; alpha-amylase; 1.
Pfam; Pr002922; isoamylase_N; 1.
Hydrolase; Complete proteon
SEQUENCE 600 AA; 66909 MW; 58
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                                                                                                                                                                                                                                                                                      181; Conservative
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NCBI_TaxID=1172;
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PubMed-11572479;
Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Noshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain?";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                   EDKREIPDPASRYQPLGVHDKSQLI---RTDYQILDLGKVKIEDLIIYELHVGTFSQEGN 118
                                                                                                                                                                                                         72 ADGTEVADPASSAQEREASGTSIVVDHAAYEWQTSSWRGRPWEEAVISELHVGCFTPEGT 131
                                                                                                                                                                                                                                   FKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEA 178
                                                                                                                                                                                                                                                 238 VEYWFKTFKIDGLRLDAVHAIFDNSPKHIL----QEIAEK-AHQLGKFVIAESDLNDPKI 292
                                                                                                                                                                                                                                                                                                                                                          249 ALYWLGHFRFDGLRLDATEQIRDTTKPHFLVALEHEVREAFAERQIHLVLEDAHRRSLL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                  GKYSRYRGRTHGAPVGD---LPPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAATL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YILSPYIPLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRL------KENNQM 450
                                                                                                                                                 3 SFGGN-IEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYII 61
                                                                                                                                                                                                                                                                                    HKRGIAVILDVVYNHIGPEGNYLLGLGP-YFSDRYKTPWGLTFNFDDRGCDQVRKFILEN
                                                                                                                                                                                                                                                                                                                                                                                   293 VKDDCGYKI--DAQWVDDFHHAVHAFITKEKDYYYQDF----GRIEDIEKTFKDVFVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                | : :| :| :| :| :| | :| | 366 AKEDNF-----SPEGSRARVPPQGRVNFLQNHDQIGNRAFGERLASLLQEDSLRVLAAM
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603646; CAC49676.1; -.
Transferase; Glycosyltransferase; Plasmid; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfolobus tokodaii.
Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
NCBL_TaxID=111955;
                                                                                   Length 601;
                                                                                   26.8%; Score 792.5; DB 16; Length
36.9%; Pred. No. 8e-45;
.ive 79; Mismatches 199; Indels
                                                024DA322A7B72C2E CRC64;
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Last annotation update)
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                                                66954 MW;
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19,
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01-DEC-2001 (TrEMBLrel.
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01-DEC-2001 (TremBLrel
PUTATIVE ALPHA-AMYLASE
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                                                 601 AA;
                                                                                                Best Local Similarity
Matches 192; Conserv
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                                   Complete proteome
SEQUENCE 601 AA
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                   DKREIPDPASRYQPLGVHDKSQLIRTDYQILDLG-KVKIEDLIIYELHVGTFSQEGNFKG 121
                                                                                                                                                                                                                                                                                                                                                                                           122 VIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKR 181
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                                                                                                                                                                 Gaps
                                                                                                                                                                                                       4 FGGN-IEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVEIDDIEENLTYSYIIE 62
                                                                                                                                                                                                                                 2 FGPSFLSENEVEFILMAPYQKKATLRLNEEKYDMEKDEKGYFRITV-NAKEGDKYSFII- 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GPEGNYLLGLG
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                                                                                                                    Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena variabilis.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
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                                                                                                                                                              Indels
EMBL; AP000984; BAB65938.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 217 AA; 25181 MW; 4A1235EC5B491CEF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ALPHA-GLUCANOTRANSFERASE /HYDROLASE.
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                                                                                                               Score 645; DB 17;
Pred. No. 1.4e-35;
; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 493; DB 2;
Pred. No. 6.8e-25;
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16.7%; Score 493;
Best Local Similarity 28.6%; Pred. No. 6.
Matches 159; Conservative 76; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of a low-temperature-induced cyanobacterium Anabaena variabilis M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 GIAVILDVVYNHIGPEGNYLLGLGPYF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; isoamylase_N.
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                                                                                                                                                          37;
                                                                                                                 21.8%;
58.9%;
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01,
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Best Local Similarity 58.9%
Matches 122; Conservative
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SEQUENCE 552 AA; 638
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: :	QY 318 TKEKDYYQDFGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFIQNHDQ 377 1 1 1 1 1 1 1 1 1	OY 378 VGNRGNGERLSILTDKTTYLMAATLYILSPYIPLIFMGEEYYE 420	RESULT 13 059242	ID 059242 PRELIMINARY; PRT; 652 AA. AC 059242; 000851; 000485; DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) DE 1,4-AlPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) DE (GLYCOGEN BRANCHING ENZYME) (1,4-ALPHA-GLUCAN BRANCHING ENZYME) DE (AMYLO-(1,4 TO 1,6)TRANSGLUCOSIDASE)		NCBL_TaxID=1422; [1]	RX MEDLINE-95031021; PubMed=7944355; RA Takata H., Takaha T., Kuriki T., Okada S., Takagi M., Imanaka T.; RT Properties and active center of the thermostable branching enzyme RT from Bacillus stearchermophilus."; RL Appl. Environ. Microbiol. 60:3096-3104(1994).	naka T. databas SIDIC I	-!- -!- EMBL Inte	IncerPro: 1rK004193; Isoamylase_Pfam; PF00128; alpha-amylase; 1. Pfam; PF02922; isoamylase, N; 1. Glycogen biosynthesis; Transfera	FT ACT_SITE 508 508 BY SIMILARITY. FT ACT_SITE 419 419 BY SIMILARITY. SQ SEQUENCE 652 AA; 76793 MW; 4591EB414A0E3FEF CRC64;	2%; Score 360; DB 2; Length 652; 3%; Pred. No. 6.3e-16;	Z; CONSEIVALLVE // NIEKNKGIFKLWAPYVN ::: : : HVINEGGKVGTRFCVWAPHAN
DD 187 GSTADLKKLVDECHQRGIRIIMDGIYNHSEASSPLTQIDHDYWYHHEPRDPDNN 240	OY 206 PYFSDRYKTPWGLFENFDDRGCDQVRKEILENVEYWFKTFKIDGLRLDAVHAIFDN 261	Qy 262 SPKH-ILQEIAEKAHQLGKFVIABSDLNDPKIVKDDCGYKIDAQWVDDFHHA 312	QY 313 VHAFITKEKDYYYQDEGRIEDIEKTFKDVFVYDGKYSRYRGRTHGAPVGDLPPRKFVVFI 372 1	OVGNRGNGERLSILTDKTYTMAATLYILSPYIPLIFMGEEY ::	QY 419 YETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSWKIDBEVL 473 I <td< td=""><td>Oy 474 DYYKOLINIRKRYNN 488 DD 452 DYHKGLIGLRKNN 464</td><td>DDFI TMTKADV. DOTT. AAO</td><td>093035, TERBELTAL 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seque 01-DEC-2001 (TrEMBLrel. 19, Last seque DEC-2001 (TrEMBLRel. 19, Last annot branching enzyme GLGB (FRAGMENT).</td><td>a new His-A ates express "; 0) to the EM K83002.1;</td><td>Sue 3es 4at</td><td>OY 52 EENLTYSYIIEDKREIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDLIIYELHVG 111 1</td><td>QY 112 TFSQEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYG 166 </td><td>QY 167 GPWELAKLVNEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPW 216 1 </td><td>Qy 217 GLTENFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHAIFDNSP 263 </td></td<>	Oy 474 DYYKOLINIRKRYNN 488 DD 452 DYHKGLIGLRKNN 464	DDFI TMTKADV. DOTT. AAO	093035, TERBELTAL 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seque 01-DEC-2001 (TrEMBLrel. 19, Last seque DEC-2001 (TrEMBLRel. 19, Last annot branching enzyme GLGB (FRAGMENT).	a new His-A ates express "; 0) to the EM K83002.1;	Sue 3es 4at	OY 52 EENLTYSYIIEDKREIPDPASRYQPLGVHDKSQLIRTDYQILDLGKVKIEDLIIYELHVG 111 1	QY 112 TFSQEGNFKGVIEKLDYLKDLGITGIELMPVAQFPGNRDWGYDGVFLYAVQNTYG 166	QY 167 GPWELAKLVNEAHKRGIAVILDVVYNHIGPEGNYLLGLGPYFSDRYKTPW 216 1	Qy 217 GLTENFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHAIFDNSP 263

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Matches 146;
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MEDLINE=97061201; PubMed=8905231;

MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hisouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

Tabata S.;
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                                                                                                                                                                                     NRDWGYDGVFLYAVQNTYGGPWELAKLVNEAHKRGIAVILDVVYNHI--GPEGNYLLGLG 205
                                                                                                                                                                                                                                ----HAIFDNS-PKHILQEIAEK--AHQLGKFVIAESDLNDPKIVKD-----DCGYKID 302
                                                                                                                                                                                                                                                         316 WPNNDRLYENPYAVEFLRKLNEAVFAYDPNALMIAEDSTDWPKVTAPTYEGGLGFNYKWN 375
                                                       ----KVKIEDLIIYELHVGTF-SQEGNFKGVIEKLD----YLKDLGITGIELMPVAQFPG 147
                                                                                                                                                                                                                                                                                       AQWVDDF------HHAVHAFITKEKDYYYQDFGRIEDIEKTFKDVFVYDGKYSRYR 352
                                                                                                                                                                                                                                                                                                                376 MGWMNDMLKYMETPPYERRHVHNQVTFSLLYAYS----ENFILPFSHDEVVHGKKS--- 427
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                                                                                                                                                                                                                                                                                                                                                                                                    410 PLIFMGEEYYETNPFFFFSDFSDPVLIKGVREGRLKENNQMIDPQSEEAFLKSKLSW--- 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                               PYF----SDRYKTPWGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAV----
IDDIEENLTYSY-IIEDKREI---PDPASRYQPLGVHDKSQLIRTD---YQILDLG----
                                                                                                                                                                                                                                                                                                                                             353 GRTHGAPVGDLPPRKFVVFIQNHDQVGNRGNG---ERLSILTDKTTYLMAATLYILSPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
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P73608;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GLYCOGEN OPERON PROTEIN GLGX.
GLGX OR SLR1857.
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InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
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EMBL; D90908; BAA17652.1; -.
HSSP; P10342; 1BF2.
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SEQUENCE 707 AA
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Length 707;

Score 333.5; DB 16; Pred. No. 4.1e-14;

11.3%; 23.1%;

Query Match Best Local Similarity

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29;
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                                                                                                                                                                                                                                                                                                                     EKLDYLKDLGITGIELMPVAQF-----PGNRD-----WGYDGVFLYAVQNTYGGPW 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 PWGLTFNFDDRG----CDQ--VRKFILENVEYWFKTFKIDGLRLDAVHAIFDNSPKHILQ 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 EIAEKAHQLGKFVIAESDLNDP-----KIVKD--DCG--YKID------AQWVDDFHH 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 AVHAFITKEKDY------YYQDFGRIEDIEKTF------KDVFVYDGKYS 349
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    Gaps
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    207:
197; Indels
                                                                                      FSFGGNIEKNKGIFKLWAPYVNSVKLKLSKKLIPMEKNDEGFFEVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VKIEDLIIYELHVGTFSQE----
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALKALINE AMYLOPULLUIANASE, PUTATIVE.
    Mismatches
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    83;
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKDLGITGIELMPV--------AQFPGNRDWGYDGVFLYAVQNTYGGP-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----WELAKLVNEAHKRGIAVILDVVYNHIGP------EGNYLLGLGPYFSDRYKTP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WGLTFNFDDRGCDQVRKFILENVEYWFKTFKIDGLRLDAVHAIFDNSPKHIL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 QEIAEKAHQLGKFVIAESDLNDPKIVKDDCGYK------IDAQWV----- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 -DDFHHAVH-------AFITKEKDYYYQDFGRIEDIEKTFKDVFVY------DGKY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRYRGRIHGAPVGDL-----PPRKFVVFIQNHDQVGNRGNGERLSILTDKTTYLMAAT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 LYILSPYIPLIFMGEEYYETNPFFFFSDFSDPYLIKGVREGRLKENNQMIDPQSEEAF-- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PFIHSGQEXGRT-----KQFRDPAYKTPVAEDKVPNKSHLLRDKDGNPFDY 983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.3%; Score 332.5; DB 16; Length 1280; Best Local Similarity 21.9%; Pred. No. 1.1e-13; Matches 152; Conservative 96; Mismatches 208; Indels 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 IDDIEE-----NLTYSYIIEDKREIP---DPASRYQPLGVHDKSQL------
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InterPro; IPR000461; Alpha_amylase.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02922; isoamylase_N; 1.
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                             Science 293:498-506(2001).
EMBL; AE007340; AAK74446.1; -.
TIGR; SP0268; -.
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